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OM nucleic - nucleic search, using sw model

Run on: April 17, 2004, 06:54:07 ; Search time 144 Seconds
(without alignments)
6405.058 Million cell updates/sec

Title: US-10-725-841-1
Perfect score: 1662
Sequence: 1 atgggctccagatctttac.....gagccactacgaaatgtga 1662

Scoring table: IDENTITY_NUC
Gapop 10_0 , Gapext 1.0

Searched: 682709 seqs, 277475446 residues

Total number of hits satisfying chosen parameters: 1365418

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents NA.*
1: /cgn2_6/prodata/2/ina/5A COMB.seq.*
2: /cgn2_6/prodata/2/ina/5B COMB.seq.*
3: /cgn2_6/prodata/2/ina/6A COMB.seq.*
4: /cgn2_6/prodata/2/ina/6B COMB.seq.*
5: /cgn2_6/prodata/2/ina/PCUS COMB.seq.*
6: /cgn2_6/prodata/2/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1452.4	87.4	1662	3	US-09-232-479-10
2	1452.4	87.4	1662	4	US-09-784-990-10
3	1452.4	87.4	2176	1	US-07-778-890A-2
4	1431.6	86.1	3825	6	5310678-2
5	1412.4	85.0	1662	2	US-08-663-566A-12
6	1412.4	85.0	1662	2	US-08-023-610-12
7	1412.4	85.0	1662	2	US-08-288-065A-12
8	1412.4	85.0	1662	2	US-08-362-240A-12
9	1412.4	85.0	1662	3	US-08-804-372A-10
10	1412.4	85.0	1662	5	PCT-US95-10245-12
11	1412.4	85.0	4177	2	US-08-484-575A-12
12	1412.4	85.0	4177	3	US-08-479-459-12
13	1412.4	85.0	4177	3	US-08-479-869-12
14	1412.4	85.0	4177	3	US-08-486-414-12
15	1412.4	85.0	4177	5	PCT-US94-01826A-12
16	1412.4	85.0	4177	5	PCT-US94-02252A-12
17	137.6	8.3	1685	1	US-08-105-483-370
18	137.6	8.3	1685	1	US-08-709-209-370
19	137.6	8.3	1685	1	US-08-458-101-370
20	117	7.0	1656	2	US-08-700-548-3
21	100.4	6.0	2136	1	US-08-321-587-1
22	92.8	5.6	2113	1	US-08-224-657-87
23	92.8	5.6	2113	4	US-09-354-138-87
24	92.8	5.6	4343	1	US-08-224-657-93
25	92.8	5.6	4343	4	US-09-354-138-93
26	92.8	5.6	4604	1	US-08-224-657-96
27	92.8	5.6	4604	4	US-09-354-138-96

28	92.8	5.6	4965	3	US-08-675-566-22	Sequence 22, Appl
29	92.8	5.6	5147	3	US-08-675-566-24	Sequence 24, Appl
30	92.8	5.6	5241	3	US-08-675-566-23	Sequence 23, Appl
31	92.8	5.6	8792	3	US-08-675-566-23	Sequence 25, Appl
32	88	5.3	2521	1	US-08-368-803-16	Sequence 16, Appl
33	88	5.3	2521	2	US-08-578-096A-18	Sequence 18, Appl
34	88	5.3	2521	3	US-08-790-517-8	Sequence 8, Appl
35	88	5.3	2521	3	US-09-240-426-18	Sequence 18, Appl
36	88	5.3	2521	3	US-09-219-932-14	Sequence 14, Appl
37	88	5.3	2521	4	US-09-362-831-8	Sequence 8, Appl
38	84.2	5.1	15894	1	US-08-348-891A-1	Sequence 1, Appl
39	84.2	5.1	15894	1	US-08-905-817-1	Sequence 1, Appl
40	82.6	5.0	1653	3	US-09-230-944-17	Sequence 17, Appl
41	82.6	5.0	1653	4	US-09-873-233A-17	Sequence 17, Appl
42	82.6	5.0	1687	1	US-08-279-700-15	Sequence 15, Appl
43	82.2	4.9	15462	3	US-09-073-492-1	Sequence 1, Appl
44	81	4.9	1653	3	US-09-230-944-19	Sequence 19, Appl
45	81	4.9	1653	4	US-09-873-233A-19	Sequence 19, Appl

ALIGNMENTS

RESULT 1
US-09-232-479-10
; Sequence 10, Application US/09232479
; Patent No. 6221362
; GENERAL INFORMATION:
; APPLICANT: AUDONNET, JEAN-CHRISTOPHE
; APPLICANT: BOUCHARDON, ANNABELLE
; APPLICANT: RIVIERE, MICHEL
; TITLE OF INVENTION: AVIAN POLYNUCLEOTIDE VACCINE FORMULA
; FILE REFERENCE: 454313-2260
; CURRENT APPLICATION NUMBER: US/09/232,479
; EARLIER FILING DATE: 1999-01-15
; EARLIER APPLICATION NUMBER: 96/09339
; EARLIER FILING DATE: 1996-07-19
; EARLIER APPLICATION NUMBER: PCT/FR97/01326
; EARLIER FILING DATE: 1997-07-16
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 10
; LENGTH: 1662
; TYPE: DNA
; ORGANISM: Newcastle disease virus
US-09-232-479-10

Query Match	87.4%	Score	1452.4	DB	3	Length	1662
Best Local Similarity	92.1%	Pred. No.	0				
Mismatches	1531	Conservative	0	Mismatches	131	Indels	0
Gaps	0						
Qy	1	ATGGGCTCCAGATCTTCTTACCAGATCCAGTACCTCTGATGCTGACCGTCCGGTCCGG	60				
Db	1	ATGGGCTCCAGATCTTCTTACCAGATCCGGTACCTCTAATGCTGATCATCCGAACCGG	60				
Qy	61	CTGGCATGATGTCGTCCTCGCAAGCTCCCTTATCGGAGGCTCTTTGAGCTGCA	120				
Db	61	CTGACACTGAGCTGTATCCCTCTGACAGCTCTTGTATGCGAGGCTCTTGGCGTCA	120				
Qy	121	GGGATGTGTGTGACGAGGACAAAGCAGTCAACATATACACCTCATCTCAGAGGTC	180				
Db	121	GGGATGTGTGTGACGAGGACAAAGCAGTCAACATATACACCTCATCTCAGAGGTC	180				
Qy	181	ATCATAGTCAAGTACTTCCCAATATGCCCCAAGAGTAAAGAGCGGTGTGCAAAAGCCCG	240				
Db	181	ATCATAGTCAAGTACTTCCCAATATGCCCCAAGAGTAAAGAGCGGTGTGCAAAAGCCCG	240				
Qy	241	TTGGAGCGGTACACAGGACATGACTTCTTGTCTACCCCTTGTGATCTTATTCGT	300				
Db	241	TTGGAGCGGTACACAGGACATGACTTCTTGTCTACCCCTTGTGATCTTATTCGT	300				
Qy	301	AGGATACAAGAGTCTGTGACTTACATCTTGGAGGAGGAAACAGGACCGCTTATAGCGCC	360				

Db 301 AGGATACAAAGAGTCTGTGACTCTCCGGAGGAAGGAGACAGAGACGCTTTTATAGTGCC 360
QY 361 ATTATCGGGGTGACGCTCTCGGGGTGCAACCGCTGCGACAGATACAGACAGCTTCGGCT 420
Db 361 ATTATCGGAGTGTAGCTCTTGGGGTGGCAGCTGCGACAGATACAGACAGCTTCGGCC 420
QY 421 CTGATACAAAGCAACCAAAATGTGCAACATCTCCGGCTTAAAGAGAGAAATGTGTCA 480
Db 421 CTGATACAAAGCAACCAAGATGCTGCAACATCTCCGGCTTAAAGAGAGAAATGTGTCA 480
QY 481 ACCAATGAGCTGTGCAACAGGTCACTGATGATATCAACTAGCAGTGGCAGTTGG 540
Db 481 ACCAATGAGCTGTGCAACAGGTCACTGATGATATCAACTAGCAGTGGCAGTTGG 540
QY 541 AAGATGCAACAAATTTGTTAATGACCAAGTTTAAATAAAGAGCTCAGGAATGACGTATA 600
Db 541 AAGATGCAACAGTTTGTAAATGACCAAGTTTAAATAAAGAGCTCAGGAATGACGTATA 600
QY 601 AAAATACCCAGAGTGTGTAGAACTCAACCTGTATCTAACTGAATGACTACAGTA 660
Db 601 AAAATGACAGAGCTGGTGTAGAACTCAACCTGTATCTAACTGAATGACTACAGTA 660
QY 661 TTCGGGCCACAATCACTCCCTGCTTAAACCAAGCTGATATCAAGCGCTTTACAA 720
Db 661 TTCGGGCCACAATCACTCCCTGCTTAAACCAAGCTGATATCAAGCGCTTTACAA 720
QY 721 CTAGCTGTGGGAATATGATTTACTTTGTGCTAAGTTAGGTAGGGAACAACCACT 780
Db 721 CTAGCTGTGGGAATATGATTTACTTTGTGCTAAGTTAGGTAGGGAACAACCACT 780
QY 781 AGCTCATTAATGTGTAGCGGCTGATCACCGCAACCCCTATTCTGTAGACTCACAGACT 840
Db 781 AGCTCATTAATGTGTAGCGGCTGATCACCGCAACCCCTATTCTGTAGACTCACAGACT 840
QY 841 CAGCTCTTGGGTATACAGTAACCTACCTCAGTCGGGAACCTGAATATATGCGTCC 900
Db 841 CAGATCTTGGGTATACAGTAACCTTGCCTTCAGTTGGGAACCTGAATATATGCGTCC 900
QY 901 ACCTACTTTGAAACCTTCTGTAGTAACTAACCAAGAGTTGCTCAGCACTCGTCCA 960
Db 901 ACCTACTTGGAGCTTATCTGTAAAGCAACCAAGGATTTGCTCAGCACTCGTCCA 960
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Db 961 AAGTGTGTAGAGGTCGGTTCGGTGATAGAACTTGACCTCATCTGTATAGAG 1020
QY 1021 ACCGATTTGGATCTATATGTACAGATAGTACATCCCTATGTCTCTGGTATTAT 1080
Db 1021 ACCGATTTGGATCTATATGTACAGATAGTACATCCCTATGTCTCTGGTATTAT 1080
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QY 1141 ACGCGGTACATGACTCTCAAGGCTCAGTTATTCGCAACTGTAAGATGCAACAATGAGA 1200
Db 1141 ACGCGATATATGGCTCTCAAGGCTCAGTTATTCGCAACTGTAAGATGCAACAATGAGA 1200
QY 1201 TGTGCAAGACCCCGGCTATCATATCGCAAAATATGAGAGAGTGTCTCTTAATAGAT 1260
Db 1201 TGTGCAAGTCCCGGCTATCATATCGCAAAATATGAGAGAGTGTCTCTTAATAGAT 1260
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Db 1261 AGGCAATCATGCAATGCTTATCTTAGCGGATAACTTTGAGGCTCAGTGGGGAATTT 1320
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Db 1321 GATGCACTTATCAAAAGATATCTCAATACAGATTTCTCAAGTATCGTGAAGGCAAT 1380
QY 1381 CTCGATATCTCGACTGAGCTTGGGAATGTCAACCACTCGGATAGTATGCTTTAGATAAG 1440
Db 1381 CTTGATATATCAACTGAGCTTGGGAATGTCAACCACTCGGATAGTATGCTTTAGATAAG 1440

RESULT 2

US-09-784-990-10
; Sequence 10, Application US/09784990
; Patent No. 6464984
; GENERAL INFORMATION:
; APPLICANT: AUDONNET, JEAN-CHRISTOPHE
; APPLICANT: BOUCHARDON, ANNABELLE
; APPLICANT: RIVIERE, MICHEL
; TITLE OF INVENTION: AVIAN POLYNUCLEOTIDE VACCINE FORMULA
; FILE REFERENCE: 454313-2260
; CURRENT APPLICATION NUMBER: US/09/784,990
; CURRENT FILING DATE: 2001-02-15
; PRIOR APPLICATION NUMBER: 96/09339
; PRIOR FILING DATE: 1996-07-19
; PRIOR APPLICATION NUMBER: PCT/FR97/01326
; PRIOR FILING DATE: 1997-07-16
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 10
; LENGTH: 1662
; TYPE: DNA
; ORGANISM: Newcastle disease virus
US-09-784-990-10

Query Match 87.4%; Score 1452.4; DB 4; Length 1662;
Best Local Similarity 92.1%; Pred. No. 0;
Matches 153; Conservative 0; Mismatches 131; Indels 0; Gaps 0;

QY 1 ATGGGCTCCAGATCTTCTACAGGATCCAGATCCAGTCTCTGTATGCTGACCGTCCGGGTCCG 60
Db 1 ATGGGCTCCAGATCTTCTACAGGATCCAGTCTCTGTATGCTGACCGTCCGGGTCCG 60
QY 61 CTGGCACTGAGTGGCTCTGTGCGACAAGCTCCCTTGTATGCGAGGCTCTTTCAGAGTCCA 120
Db 61 CTGACACTGAGTGGTATCCGCTGACAAAGCTCTCTGATGCGAGGCTCTTTCAGAGTCCA 120
QY 121 GGGATTTGCTGACAGAGCAAGCAAGCTCAACATATACACCTCATCTCAGAGGCTCA 180
Db 121 GGGATCTGTTAAGAGAGATAAGCAAGCTCAACATATACACCTCATCTCAGAGAGGCTCA 180
QY 181 ATCATAGTCAAGTTACTTCCCAAAATATGCCCAAGATAAAGAGGCTGTGCAAAAGCCCG 240
Db 181 ATCATAGTTAAGTTACTTCCCGAATATGCCCAAGATAAAGAGGCTGTGCAAAAGCCCG 240
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Db 241 TTGAGGCGGTACAAAGGACATTTGACTATCTTGTGCTCACTTGTGATTTCTATTCGT 300
QY 301 AGGATACAGAGTCTGTGACTACTCTGAGGAGGGAACAGGAGCCCTTATAGGCGCC 360
Db 301 AGGATACAGAGTCTGTGACTACTCTGAGGAGGGAACAGGAGCCCTTATAGGCGCC 360
QY 361 ATTATCGGCGGTGACGCTCTCGGGGTGCAACCGCTGCAAGATACAGAGCTTCGGCT 420
Db 361 ATTATCGGCGGTGACGCTCTCGGGGTGCAACCGCTGCAAGATACAGAGCTTCGGCT 420

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QY 421 CTGATACAGCGCAACCAAAATGCTGCCAATCCTCCGGCTTAAAGAGAGAAATTGCTGCA 480
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Db 481 ACCAATGAGCGTGTGCACGAGGTCACTGATGGAATATCAAACTAGCAGTGGCAGTAGGG 540
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Db 541 AAGATCGACGAATTTGTTCAATGACCAAGTTTCAATAATACAGCGCAAGAAATTGGACTGTATA 600
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Db 721 CTAGCTGGTGGTAAATATGGAATTAATTTGTTGACTAAGTTAGGTAGGGAACAACCAACTC 780
QY 781 AGCTCTAATTTGGTAGCGGCTGATCACCGGCAACCCATTCTGTAGCACTCAGACACT 840
Db 781 AGCTCTAATTTGGTAGCGGCTGATCACCGGCAACCCATTCTGTAGCACTCAGACACT 840
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Db 841 CAGATCTTGGGTATACAGGTAACTTTCCTTTCAGTTGGGAACTGGAATATATGCGTGCC 900
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Db 1021 ACCGATTTGGATTTATCTGTAAGAAATAGTGACATTCCTATGCTCTCTGGTATTAT 1080
QY 1081 TCCTGTTTGAGCGCAATACATCGGCTTGCATGTATTCAAAGACTGAAGCGCACTCACT 1140
Db 1081 TCCTGTTGAGCGCAATACATCGGCTTGCATGTATTCAAAGACTGAAGCGCACTCACT 1140
QY 1141 ACCGCTGATGACTCTCAAGGCTCAGTTATTGCCAACTGTAGATGACAACTGTAGA 1200
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Db 1201 TGTGCAGATCCCCAGGTATCATATCGCAAAATATGGAAGAGTGTGTCTCTAAATAGAT 1260
QY 1261 AGGCAATCATGCAATGCTCTATCTTATAGACGGAATAAATTTGAGGCTCAGTGGGAATTT 1320
Db 1261 AGGCACTCATGCAAGCTCTTATCTTATAGACGGAATAAATCTGAGGCTCAGTGGGAATTT 1320
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Db 1321 GATGCAACCTATCAAGAATAATCTCTATCTAGATTTCTCAAGTAATCTGACAGGCAAT 1380
QY 1381 CTCGATATCTCGACTGAGCTTGGGAATGTCAACAACTCGAATAAGTAATGCTTTAGATAAG 1440
Db 1381 CTTGATATATCAACTGAGCTTGGGAATGTCAACAACTCAATAAGTAATGCTTGAATAAG 1440
QY 1441 TTAGAGGAAGCAACAGCAAACTAGACAAGGTCAATGTCAAACTGCACAGCACATCCGCT 1500
Db 1441 TTAGAGGAAGCAACAGCAAACTAGACAAGGTCAATGTCAAACTGCACAGCACATCTGCT 1500
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Db 1501 CTCATTACCTATACGCTTTTAACTGTCAATATCTTGTGTTGGTATATCTAGCCTGGTT 1560
QY 1561 CTAGCATGCTACCTGATGTACAAGCAAAAGGCGCAACAGAAAGACCTTGTGTTGGTTGGG 1620
Db 1561 CTAGCATGCTACCTGATGTACAAGCAAAAGGCGCAACAAAGACCTTGTGTTGGTTGGG 1620
QY 1621 AATAATACCTGTGATCAGATGAGAGCCACTACGAAAATGTGA 1662
Db 1621 AATAATACCTTGTATCAGATGAGAGCCACTACAAAATATGA 1662
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RESULT 3

US-07-778-890A-2

; Sequence 2, Application US/07778890A

; Patent No. 5266489

; GENERAL INFORMATION:

; APPLICANT: 1.REY-SENELONGE Arielle

; APPLICANT: 2.KOHN Gilla

; TITLE OF INVENTION: recombinant herpes viruses,in particular for the

; TITLE OF INVENTION: production of vaccines,process for preparing them,plasmids pro

; TITLE OF INVENTION: during this process and vaccines obtained.

; NUMBER OF SEQUENCES: 7

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Larson and Taylor

; STREET: 727 Twenty-Third Street,South

; CITY: Arlington

; STATE: Virginia

; COUNTRY: USA

; ZIP: 22202

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette-5.25 inch,360Kb storage

; COMPUTER: IBM PC/XT/AT or compatibles

; OPERATING SYSTEM: PC-DOS or MS-DOS version 2.2 or above

; SOFTWARE: KEDIT or any ASCII Text Editor

; CURRENT APPLICATION DATA: 07/778,890

; APPLICATION NUMBER: US/07/778,890A

; FILING DATE: 19920103

; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: FR9003105,PCT/FR/91/00184

; FILING DATE: 12-MAR-1990,07-MAR-1991

; INFORMATION FOR SEQ ID NO: 2:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 2176 base pairs

; TYPE: NUCLEIC ACID

; STRANDEDNESS: double

; TOPOLOGY: circular

; MOLECULE TYPE: cDNA to genomic RNA

; HYPOTHETICAL: yes

; ANTI-SENSE: no

; ORIGINAL SOURCE:

; ORGANISM: Newcastle disease virus (NDV)

; STRAIN: Texas strain

; INDIVIDUAL ISOLATE: chicken

; IMMEDIATE SOURCE:

; LIBRARY: plasmid

; CLONE: pNDV 108

; FEATURE:

; NAME/KEY: part of matrix protein gene and fusion protein gene

; LOCATION: from to description

; LOCATION: 1 271 matrix protein gene

; LOCATION: 431 2092 fusion protein gene

US-07-778-890A-2

Query Match

Best Local Similarity 87.4%; Score 1452.4; DB 1; Length 2176;

Matches 1531; Conservative 0; Mismatches 131; Indels 0; Gaps 0;

QY 1 ATGGGCTCCAGATCTTCTTACAGGATCCCAAGTACCTCTGATGCTGACCGTCCGGTCCG 60

Db 431 ATGGGCTCCAGATCTTCTTACAGGATCCCGGTACCTCTAATGCTGATCATCCGAACCGG 490

O 61 CTGGCACTGAGTTGGTCTGTGCGCAAGCTCCCTTGATGGCAGGCTCTTGCAGTGA 120
Db |||||
491 CTGACACTGAGCTGTATCCGTCTGCAAGCTCTCTTGATGGCAGGCTCTTGGCGTGA 550
QY |||||
121 GGGATTGGTGCACAGGAGCAAAAGCAGTCAACATATACACCTCATCTCAGACAGGCTCA 180
Db |||||
551 GGGATCGTGTAAACAGGAGTAAGCAGTCAACATATACACCTCATCTCAGACAGGCTCA 610
QY |||||
181 ATCATAGTCAAGTTACTCCCAATATGCCAAAGATTAAGAGCGGTGTGCAAAAGCCCG 240
Db |||||
611 ATCATAGTTAAGTTACTCCCGAATATGCCAAGGCAAAAGAGTGTGTGCAAAAGCCCG 670
QY |||||
241 TTGGAGGCGTCAACAGGACATTTGACTCTTTGCTCACCCTTGGTGGATTTCTATTGCT 300
Db |||||
671 TTGGAGGCGTCAACAGGACATTTGACTCTTTACTCACCCTTGGTGGATTTCTATTGCT 730
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301 AGGATACAGAGTGTGTGACTCATCTGGAGGAGGAAACAGGAGCGCTTTATAGCGCC 360
Db |||||
731 AGGATACAGAGTGTGTGACTCATCTCGGAGGAGGAGACAGAGCGCTTTATAGTGGC 790
QY |||||
361 ATTATCGGCGTGCAGCTCTCGGGTTCGACCGCTGACAGATTAACAGCAGCTTCGGCT 420
Db |||||
791 ATTATCGGCGTGCAGCTCTCGGGTTCGACCGCTGACAGATTAACAGCAGCTTCGGCT 850
QY |||||
421 CTGATACAGGCAACCAAAATGCTGCCAATCTCCTCGGCTTAAAGAGAGATTTGCTGCA 480
Db |||||
851 CTGATACAGGCAACCAAGATGCTGCCAATCTCCTCGGCTTAAAGAGAGATTTGCTGCA 910
QY |||||
481 ACCAATGAGGTGTGCAAGAGTCACTGATGATTATCAAACTAGCAGTGGCAGTTGGG 540
Db |||||
911 ACCAATGAGGTGTGCAAGAGTCACTGACGATTATCAAACTAGCAGTGGCAGTTGGG 970
QY |||||
541 AAGATGCAAGATTTGTTAATGACAGTTTAAATAAAGCTCAGAAATGACGTGTATA 600
Db |||||
971 AAGATGCAAGATTTGTTAATGACAGTTTAAATAAAGCTCAGAAATGACGTGTATA 1030
QY |||||
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Db |||||
1031 AAAATTGACAGCAGGTCGGTGTAGAACTCAACCTGTATCTAACTGAATGACTACAGTA 1090
QY |||||
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Db |||||
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QY |||||
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Db |||||
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Db |||||
1211 AGCTCAATTAATGGTAGGCGCTGTATCCCGCAACCTTATCTGTAGCTTCAGACT 1270
QY |||||
841 CAGCTCTTGGTATACAGTAAACCTTACCTCAGTCGGGAACCTGAATTAATGGTGGC 900
Db |||||
1271 CAGCTCTTGGTATACAGTAAACCTTACCTCAGTCGGGAACCTGAATTAATGGTGGC 1330
QY |||||
901 ACCTACTTGGAAACCTTGTCTGTAAGTAAACCAAGGATTTGCCCTCAGCACTGTCCTCA 960
Db |||||
1331 ACCTACTTGGAAACCTTGTCTGTAAGTAAACCAAGGATTTGCCCTCAGCACTGTCCTCA 1390
QY |||||
961 AAGTGTGTGTAAGGTCGGTTCCGTGTAGAGAACTTGACACCTCATCTGTATAGAG 1020
Db |||||
1391 AAGTGTGTGTAAGGTCGGTTCCGTGTAGAGAACTTGACACCTCATCTGTATAGAG 1450
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Db |||||
1451 ACCGATTTGGATCTATATTTGTAAGAAATAGTGAATTTCCCTATGTCTCTGGTATTAT 1510
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1511 TCCTGTTTGGCGGCAATACATCGGCTTGCATGTACTCGAAGCTGGAAGGCGCACTCACT 1570

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1571 ACGCATATATGGCTCTCAAGGCTCAGTTATTGCCAAGCTTAAGTGAACAATGATGA 1630
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1201 TGTGCAAGCCCCCGGCTATCATATCGGAAATATGGAAGAGCTGTCTCTTAATAGAT 1260
Db |||||
1631 TGTGCAAGCCCCCGGCTATCATATCGGAAATATGGAAGAGCTGTCTCTTAATAGAT 1690
QY |||||
1261 AGGCAATCATGCAATGTCTCTATCTTAGACGGAATAACTTTGAGGCTAGTGGGGAATTT 1320
Db |||||
1691 AGGCAATCATGCAATGTCTCTATCTTAGACGGAATAACTTTGAGGCTAGTGGGGAATTT 1750
QY |||||
1321 GATGCAACTTATCAAAAGATATCTCAATACAGATTTCTCAAGTAACTCGTGACAGCAAT 1380
Db |||||
1751 GATGCAACTTATCAAAAGATATCTCTATACAGATTTCTCAAGTAACTTAGTGACAGCAAT 1810
QY |||||
1381 CTCGATATCTCGACTGAGCTTGGGAATGTCAACCACTCGATAAGTAATGCTTTAGATAAG 1440
Db |||||
1811 CTTGATATCAACTGAGCTTGGGAATGTCAACCACTCAATAAGTAATGSCCTGAATAAG 1870
QY |||||
1441 TTAGAGGAAGCAACAGCAACTAGACAAAGTCAATGTCAAACTGACACGACATCCGCT 1500
Db |||||
1871 TTAGAGGAAGCAACAGCAACTAGACAAAGTCAATGTCAAACTGACACGACATCCGCT 1930
QY |||||
1501 CTCATCACTATATCGTTTAACTGTCTATCTCTTGTGTTGTTGTTGTTGTTGTTGTT 1560
Db |||||
1931 CTCATCACTATATCGTTTAACTGTCTATCTCTTGTGTTGTTGTTGTTGTTGTTGTT 1990
QY |||||
1561 CTAGCATCTACTGTATGATCAAGCAAAAGGCGCAACAGAGACCTTGTGTTGTTGTTGTT 1620
Db |||||
1991 CTAGCATCTACTGTATGATCAAGCAAAAGGCGCAACAGAGACCTTGTGTTGTTGTTGTT 2050
QY |||||
1621 AATAATACCTGTGATCAGATGAGGCGCACTAGCAAAATGTGA 1662
Db |||||
2051 AATAATACCTGTGATCAGATGAGGCGCACTAGCAAAATGTGA 2092

RESULT 4
5310678-2
; Patent No. 5310678
; APPLICANT: Bingham, Richard W.; Chambers, Philip; Emerson, Peter
; T.; Millar, Neil S.
; TITLE OF INVENTION: NEWCASTLE DISEASE VIRUS GENE CLONES
; NUMBER OF SEQUENCES: 3
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/438,945
; FILING DATE: 17-NOV-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 885,765
; FILING DATE: 15-JUL-1986
; SEQ ID NO: 2:
; LENGTH: 3825
5310678-2

Query Match 86.1%; Score 1431.6; DB 6; Length 3825;
Best Local Similarity 91.3%; Pred. No. 0;
Matches 1518; Conservative 0; Mismatches 144; Indels 0; Gaps 0;

QY 1 ATGGGCTCCAGATCTTCTACAGGATCCAGTACTCTGTGCTGACCGTCCGGTCCGC 60
Db |||||
47 ATGGGCTCCAGATCTTCTACAGGATCCAGTACTCTGTGCTGACCGTCCGGTCCGC 106
QY |||||
61 CTGGCACTGAGTTGGTCTGTGCGCAAGCTCCCTTGTATGAGCGGCTCTTGCAGCTGA 120
Db |||||
107 CTGGTACTGAGTTGGTCTGTGCGCAAGCTCCCTTGTATGAGCGGCTCTTGCAGCTGA 166
QY |||||
121 GGGATTGTGTGACAGGAGCAAAAGCAGTCAACATATACACCTCATCTCAGACAGGCTCA 180
Db |||||
167 GGAATTTGGTAAACAGGAGCAAAAGCAGTCAACATATACACCTCATCTCAGACAGGATCA 226
QY |||||
181 ATCATAGTCAAGTTACTCCCAATATGCCCAGAAAGATTAAGAGGCGGTGTGCAAAAGCCCG 240
Db |||||
227 ATCATAGTCAAGTTACTCCCAATATGCCCAGAAAGCTGCCCAGGATAGGAGGCGCATGTG 286

241 TTGGAGCGGTACACAGGACATTGACTATCTTTGCTACACCCCTTGGTGATCTATTCGT 300
Db |||||
287 TTGGATGCATACACAGGACATTGACACCTTTGCTACACCCCTTGGTGATCTATCCGT 346
Qy |||||
301 AGGATACAGAGCTGTGACTACATCTGGAGGAGGAAACAGGAGCGCCTTATAGCGCC 360
Db |||||
347 AGGATACAGAGCTGTGACTACATCTGGAGGAGGAGACAGAAACGCTTTATAGCGCC 406
Qy |||||
361 ATTATCGGCGGTGAGCTCTCGGGGTTGCAACCGCTGCACAGATAACAGCAGCTTCGGCT 420
Db |||||
407 ATTATCGGCGGTGAGCTCTCGGGGTTGCAACCGCTGCACAAATAACAGCGCGCAGCT 466
Qy |||||
421 CTGATACAGCCAAACCAAAATGCTGCCAATCTCTCGGCTTAAAGAGAGAAATGCTGCA 480
Db |||||
467 CTGATACAGCCAAACCAAAATGCTGCCAATCTCTCGGCTTAAAGAGAGCAATGCGCA 526
Qy |||||
481 ACCAATGAGGCTGTGACGAGGTCAGTGATGGATTATCAAACTAGCAGTGCGAGTTGGG 540
Db |||||
527 ACCAATGAGGCTGTGATGAGGTCAGTGATGGATTATCGCAACTAGCAGTGCGAGTTGGG 586
Qy |||||
541 AAGATGAGCAATTTGTTAATGACCAATTTAATAAAACAGCTCAGGAATTTGACTGATA 600
Db |||||
587 AAGATGAGCAATTTGTTAATGACCAATTTAATAAAACAGCTCAGGAATTTAGGCTGATC 646
Qy |||||
601 AAAATGAGGCTGTGACGAGGTCAGTGATGGATTATCAAACTAGCAGTGCGAGTTGGG 660
Db |||||
647 AGAATGACAGCAAGTTGTTGAGAGTCAAGCTGACCTAACCGAAATTTGACTACAGTA 706
Qy |||||
661 TTCGGGCGCAAAATCACTTCCCTGCTTAAACCGAGCTGACTATCAAGGCGCTTTACAAT 720
Db |||||
707 TTCGGGCGCAAAATCACTTCCCTGCTTAAACCGAGCTGACTATCAAGGCGCTTTACAAT 766
Qy |||||
721 CTAGCTGTGGGAATTTGTTAATGACCAATTTAATAAAACAGCTCAGGAATTTGACTGATA 780
Db |||||
767 CTAGCTGTGGGAATTTGTTAATGACCAATTTAATAAAACAGCTCAGGAATTTGACTGATA 826
Qy |||||
781 AGCTCATTAATGTTAGTGGCTGTGATGAGGTCAGGCAACCTTATCTGACGACTACAGACT 840
Db |||||
827 AGCTCATTAATGTTAGTGGCTGTGATGAGGTCAGGCAACCTTATCTGACGACTACAGACT 886
Qy |||||
841 CAGCTTGTGGTATACAGGTAACCTTACCTCAGTGGGAACTTGAATAATATGCGTGCC 900
Db |||||
887 CAAGTGTGGTATACAGGTAACCTTACCTCAGTGGGAACTTGAATAATATGCGTGCC 946
Qy |||||
901 ACCTACTTGAACCTTATCTGTAAGTACACCAAGGATTTGCTCAGCACTGTCCTCA 960
Db |||||
947 ACCTACTTGAACCTTATCTGTAAGTACACCAAGGATTTGCTCAGCACTGTCCTCA 1006
Qy |||||
961 AAGTGTGTGATGAGGTCGGTTCGGTATAGAGAACTTGACACCTCATCTGATAGAG 1020
Db |||||
1007 AAGTGTGTGATGAGGTCGGTTCGGTATAGAGAACTTGACACCTCATCTGATAGAG 1066
Qy |||||
1021 ACCGATTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1080
Db |||||
1067 ACCGATTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1126
Qy |||||
1081 TCTGTTTGAAGCGCAATACATCGGCTTGTGATGATGATGATGATGATGATGATGATGAT 1140
Db |||||
1127 TCTGTTTGAAGCGCAATACATCGGCTTGTGATGATGATGATGATGATGATGATGATGAT 1186
Qy |||||
1141 ACCGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1200
Db |||||
1187 ACCGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1246
Qy |||||
1201 TGTGACAGCCCGGGTATCATATCGCAAAATTTATGGAAGAGCTGTGTCTCTAATAGAT 1260
Db |||||
1247 TGTGTAACCCCGGGTATCATATCGCAAAATTTATGGAAGAGCTGTGTCTCTAATAGAT 1306
Qy |||||
1261 AGGCAATCATGCAATGCTTCTTATGACGGAATTAATTTAGGCTCAGTGGGGAATTT 1320
Db |||||
1307 AAGCAATCATGCAATGCTTCTTATGACGGAATTAATTTAGGCTCAGTGGGGAATTT 1366

Qy 1321 GATGCAACTTATCAAAAGATATCTCAATACAGATTTCTCAAGATTCGTGACAGGCAAT 1380
Db |||||
1367 GATGCAACTTATCAAAAGATATCTCAATACAGATTTCTCAAGATTAATAACAGGCAAT 1426
Qy 1381 CTGATATCTGAGCTGAGCTTGGGAATGTCAACAACTCGAATAAGTATGCTTTAGATAAG 1440
Db |||||
1427 CTGATATCTGAGCTGAGCTTGGGAATGTCAACAACTCGAATAAGTATGCTTTAGATAAG 1486
Qy 1441 TTAGAGAAAGCAACAGCAAACTAGACAAAGGTCAATGTCAAACTGACCAAGCAATCGCT 1500
Db |||||
1487 TTAGAGAAAGCAACAGCAAACTAGACAAAGGTCAATGTCAAACTGACCAAGCAATCGCT 1546
Qy 1501 CTGATCACTATATCTGTTTAACTGTATATCTCTGTTTGTGTTATGCTTATGCTTGGT 1560
Db |||||
1547 CTGATCACTATATCTGTTTAACTGTATATCTCTGTTTGTGTTATGCTTATGCTTGGT 1606
Qy 1561 CTGATCACTATATCTGTTTAACTGTATATCTCTGTTTGTGTTATGCTTATGCTTGGT 1620
Db |||||
1607 CTGATCACTATATCTGTTTAACTGTATATCTCTGTTTGTGTTATGCTTATGCTTGGT 1666
Qy 1621 AATAATACCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1680
Db |||||
1667 AATAATACCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1708

RESULT 5

US-08-663-566A-12
; Sequence 12, Application US/08663566A
; Patent No. 5853733
; GENERAL INFORMATION:
; APPLICANT: Cochran, Mark D
; APPLICANT: Macdonald, Richard D
; TITLE OF INVENTION: Recombinant Herpesvirus of Turkeys
; TITLE OF INVENTION: and Uses Thereof
; NUMBER OF SEQUENCES: 56
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: John P. White
; STREET: 1185 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/663,566A
; FILING DATE: June 13, 1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: White, John P
; REGISTRATION NUMBER: 28,678
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212)278-0400
; TELEFAX: (212)391-0526
; TELEX: 422523
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1662 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..1662
; US-08-663-566A-12

Query Match 85.0%; Score 1412.4; DB 2; Length 1662;

Best Local Similarity 90.6%; Pred. No. 0;
Matches 1506; Conservative 0; Mismatches 156; Indels 0; Gaps 0;

QY 1 ATGGGCTCCAGATCTTACAGGATCCAGTACCTCTGATGCTGACCGTCGGGTCGG 60
DB 1 ATGGGCTCCAGATCTTACAGGATCCAGTACCTCTGATGCTGACCGTCGGGTCGG 60
QY 61 CTGGCACTGAGTGTGCTGTCGCAAGCTCCCTTTGATGGCAGGCTCTTGCAGTGA 120
DB 61 CTGGCACTGAGTGTGCTGTCGCAAGCTCCCTTTGATGGCAGGCTCTTGCAGTGA 120
QY 121 GGGATTTGGTACAGGAGCAAGAGAGTCAACATATACCTCTATCTCAGAGGTC 180
DB 121 GGGATTTGGTACAGGAGCAAGAGAGTCAACATATACCTCTATCTCAGAGGTC 180
QY 181 ATCATAGTCAAGTCTTCTCCCAATATGCCCAAGATTAAGAGCGGTGTGCAAAAGCCCG 240
DB 181 ATCATAGTCAAGTCTTCTCCCAATATGCCCAAGATTAAGAGCGGTGTGCAAAAGCCCG 240
QY 241 TTGGAGGCGTCAACAGGACATTTGACTCTTTGCTCACCCTCTTGGTGAATCTTATCGT 300
DB 241 TTGGAGGCGTCAACAGGACATTTGACTCTTTGCTCACCCTCTTGGTGAATCTTATCGT 300
QY 301 AGGATACAAGTCTGTGACTACATCTGGAGAGGGAACAGGAGCGCTTATAGGCGCC 360
DB 301 AGGATACAAGTCTGTGACTACATCTGGAGAGGGAACAGGAGCGCTTATAGGCGCC 360
QY 361 ATTATCGGCGGTGAGCTCTCGGGGTGCAACCGCTGCACAGATTAACAGCAGCTTCGGCT 420
DB 361 ATTATCGGCGGTGAGCTCTCGGGGTGCAACCGCTGCACAGATTAACAGCAGCTTCGGCT 420
QY 421 CTGATACAAGCCCAACAAATCTGCCAATCTCCCGCTTTAAAGAGAGATTTGCTGA 480
DB 421 CTGATACAAGCCCAACAAATCTGCCAATCTCCCGCTTTAAAGAGAGATTTGCTGA 480
QY 481 ACCAATGAGCTGTGCAAGAGTCACTGATGATTTATCAACATGAGGAGTGGG 540
DB 481 ACCAATGAGCTGTGCAAGAGTCACTGATGATTTATCAACATGAGGAGTGGG 540
QY 541 AAGATGCAAGATTTGTTAATGACCAAGTTTAAACAGCTCAGGAATGACATGATA 600
DB 541 AAGATGCAAGATTTGTTAATGACCAAGTTTAAACAGCTCAGGAATGACATGATA 600
QY 601 AAAATACCCAGAGTGGTGTAGACTCAACCTGTATCTAACTGAATGACTACAGTA 660
DB 601 AAAATACCCAGAGTGGTGTAGACTCAACCTGTATCTAACTGAATGACTACAGTA 660
QY 661 TTGGGCGCACAACTCACTCCCTGCTTAAACAGCTGACTATCCAGGCGCTTTACAT 720
DB 661 TTGGGCGCACAACTCACTCCCTGCTTAAACAGCTGACTATCCAGGCGCTTTACAT 720
QY 721 CTAGCTGGTGGGAATATGGAATTAATTTGACTAAGTGTAGGTAGGGAACCAACTC 780
DB 721 CTAGCTGGTGGGAATATGGAATTAATTTGACTAAGTGTAGGTAGGGAACCAACTC 780
QY 781 AGCTCAATTAATTTGGTGGGCTGTATCCCGCAACCTTATCTGTACACTCAGACT 840
DB 781 AGCTCAATTAATTTGGTGGGCTGTATCCCGCAACCTTATCTGTACACTCAGACT 840
QY 841 CAGCTCTTGGGTATACAGTAACTTACCTCAGTCCGGGACCTGAATATGCTGCC 900
DB 841 CAGCTCTTGGGTATACAGTAACTTACCTCAGTCCGGGACCTGAATATGCTGCC 900
QY 901 ACCTACTTTGGAACCTTGTCTGAAGTACAACCAAGGATTTGCTCAGCACTCCGCCA 960
DB 901 ACCTACTTTGGAACCTTGTCTGAAGTACAACCAAGGATTTGCTCAGCACTCCGCCA 960
QY 961 AAGGTGGTGAAGAGTGGTTCCTGTATAGAGAACTTGACACCTCTACTGTATAGAG 1020
DB 961 AAGGTGGTGAAGAGTGGTTCCTGTATAGAGAACTTGACACCTCTACTGTATAGAG 1020
QY 1021 ACCGATTTGGATCTATATTGTACAAGATAGTACATCCCTATGCTCCTGGTATTAT 1080
DB 1021 ACCGATTTGGATCTATATTGTACAAGATAGTACATCCCTATGCTCCTGGTATTAT 1080

RESULT 6

US-08-023-610-12
; Sequence 12, Application US/08023610
; Patent No. 5928648
; GENERAL INFORMATION:
; APPLICANT: Cochran Ph.D, Mark D
; TITLE OF INVENTION: Recombinant Herpesvirus of Turkeys
; TITLE OF INVENTION: and Uses Thereof
; NUMBER OF SEQUENCES: 47
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: John P. White
; STREET: 30 Rockefeller Plaza
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10112
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/023,610
; FILING DATE: February 26, 1993
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: White Esq, John P
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 977-9550

```
; TELEFAX: (212) 664-0525
; TELEX: 422523
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1662 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..1662
; US-08-023-610-12

Query Match      85.0%; Score 1412.4; DB 2; Length 1662;
Best Local Similarity 90.6%; Pred. No. 0;
Matches 1506; Conservative 0; Mismatches 156; Indels 0; Gaps 0;

QY 1 ATGGGCTCCAGATCTTCTACAGGATCCAGTACCTCTGATGCTGACGGTCCGGTCCGG 60
DB 1 ATGGGCTCCAGATCTTCTACAGGATCCAGTACCTCTGATGCTGACGGTCCGGTCCGG 60
QY 61 CTGGCACTGAGTTGCGTCTGTCCGACAAAGCTCCCTTGATGGCAGGCGCTCTTGCAAGTGA 120
DB 61 CTGGTACTGAGTTGCACTCTGTCCGGCAAACTCCATTGATGGCAGGCGCTCTTGCAAGTGA 120
QY 121 GGAATTGTGGTTACAGGAGACAAAGCAGTCAACATATACACCTCATCCGACAGGATCA 180
DB 121 GGAATTGTGGTTACAGGAGACAAAGCAGTCAACATATACACCTCATCCGACAGGATCA 180
QY 181 ATCATAGTCAAGTTACTCCCAATATATGCCCAAGATTAAGAGGCGGTGCAAAAGCCCG 240
DB 181 ATCATAGTCAAGTTACTCCCAATATATGCCCAAGATTAAGAGGCGGTGCAAAAGCCCG 240
QY 241 TTGGAGCGGTACAAAGCAATGACTTCTGCTCACCCCTCTGCTGATGCTCTATTTCGT 300
DB 241 TTGGATGCAATACAGGACATGACCACTTTGCTCACCCCTCTGCTGATGCTCTATTTCGT 300
QY 301 AGGATACAAGAGTCTGTGACTTACTCTGGAGGAGGAAACAGGACGCTTTATAGGCGCC 360
DB 301 AGGATACAAGAGTCTGTGACTTACTCTGGAGGAGGAGACAGGCGGCTTTATAGGCGCC 360
QY 361 ATTATCGCGGTGACGCTCTCGGGTTGCAACCGCTGCAAGATTAAGAGGCGGTGCGCT 420
DB 361 ATTATCGCGGTGAGGCTCTGCGGGTTGCAACTCGCGGCAAAATTAAGAGGCGGTGCGCT 420
QY 421 CTGATACAAGCAACCAAAATGCTGCCAAATCTCCGGCTTAAAGAGAGAAATGCTGCA 480
DB 421 CTGATACAAGCAACCAAAATGCTGCCAAATCTCCGGCTTAAAGAGAGCAATGCTGCA 480
QY 481 ACCAATGAGGTGTGACAGGTCCTGATGATGATTAACAACCTAGCAGTGGCAAGTTGGG 540
DB 481 ACCAATGAGGTGTGATGAGTCACTGACGAGTATTCGCAACTAGCAGTGGCAAGTTGGG 540
QY 541 AAGATGAGCAATTTGTTATGACCACTTTAATAAAGAGTCAAGATGAGGATGAGTATA 600
DB 541 AAGATGAGCAAGTTGTTATGACCAATTTAATAAAGAGTCAAGATGAGGATGAGTATA 600
QY 601 AAAATTACCCAGCAGGTTGGTGTAGAATCACTCACTGATCTAATGATGATGATGATGAT 660
DB 601 AAAATTGACAGCAAGTTGGTGTAGAATCACTCACTGATCTAATGATGATGATGATGAT 660
QY 661 TTGGGGCCAAATCACTTCCCTCCCTTAACCCAGCTGACTATCCAGGCGCTTTACAAT 720
DB 661 TTGGGACCAAAATCACTTCCCTCCCTTAACCAAGCTGACTATTCAGGCGCTTTACAAT 720
QY 721 CTAGCTGGTGGATATGAGTACTTGTGATGATGATGATGATGATGATGATGATGATGAT 780
DB 721 CTAGCTGGTGGATATGAGTACTTGTGATGATGATGATGATGATGATGATGATGATGAT 780
QY 781 AGCTCATTAATTGGTAGCGGCTGATCACCGGCAACCTTCTTGTGAGTACACAGT 840
DB 781 AGCTCATTAATTGGTAGCGGCTGATCACCGGCAACCTTCTTGTGAGTACACAGT 840
QY 841 CAGCTCTTTGGGTATACAGGTAACCTTACCTCAGTCGGGAACCTGAATAATATGCGTGC 900
DB 841 CAACTCTTTGGGTATACAGGTAACCTTACCTCAGTCGGGAACCTTAAATAATATGCGTGC 900
QY 901 ACCTACTTGAACCTTGTCTGTAAGTACAAACCAAGGATTTGCTCAGCACTGCTGCCA 960
DB 901 ACCTACTTGAACCTTATCCGTAAGCAACCAAGGATTTGCTCAGCACTGCTGCCA 960
QY 961 AAGTGTGTATGAAGTTCGGTTCGGTATGAAGAAGTTCGACACCTCATCTGATATAGAG 1020
DB 961 AAGTGTGTATGAAGTTCGGTTCGGTCTGTGATGAAGAAGTTCGACACCTCATCTGATATAGAG 1020
QY 1021 ACCGATTGGATCTATATTTGTAAGAAGTATGATGATGATGATGATGATGATGATGAT 1080
DB 1021 ACTGACTTAGATTTATATTTGTAAGAAGTATGATGATGATGATGATGATGATGATGAT 1080
QY 1081 TCCTGTTGAGCGGCAATACATCGGCTGTATGCTCAAGAGCCGAAGCGGCACTTACT 1140
DB 1081 TCCTGTTGAGCGGCAATACATCGGCTGTATGCTCAAGAGCCGAAGCGGCACTTACT 1140
QY 1141 ACGCGGTACATGACTCTCAAGAGCTCAGTTTATGCGCAACTGTAAAGATGACAAATGATGA 1200
DB 1141 ACACCATATATGACTATCAAGGCTCAGTCTCGTAACTGCAAGATGACAAATGATGA 1200
QY 1201 TGTGACAGCCCCGGGTATCATATCGCAAAATTTATGGAAGAGTGTCTCTTAATAGAT 1260
DB 1201 TGTGTAACCCCCGGGTATCATATCGCAAAATTTATGGAAGAGTGTCTCTTAATAGAT 1260
QY 1261 AGCAATCATGCAATGCTCTATCTTAGAGCGGATTAATTTAGGCTCAGTGGGGAATTT 1320
DB 1261 AAACAATCATGCAATGCTCTATCTTAGAGCGGATTAATTTAGGCTCAGTGGGGAATTT 1320
QY 1321 GATGCAACTTATCAAAAGATATCTCAATCAAGATTTCTCAAGTAATTCGTGACAGGCAAT 1380
DB 1321 GATGTAATTTATCAAGAGATATCTCAATCAAGATTTCTCAAGTAATTAATCAAGGCAAT 1380
QY 1381 CTGATATCTGACTGAGCTTGGGAATGTCAAACAATGATAGTAAATGCTTTAGATAG 1440
DB 1381 CTTGATATCTCACTGAGCTTGGGAATGTCAAACAATGATAGTAAATGCTTTAGATAG 1440
QY 1441 TTAGAGAAAGCAACAGCAACTAGCAAGTCAATGCTCAAACTGACAGCACTCGCT 1500
DB 1441 TTAGAGAAAGCAACAGCAACTAGCAAGTCAATGCTCAAACTGACAGCACTCGCT 1500
QY 1501 CTGATCACTATATCGTTTAACTGTCAATCTCTTCTTTTGTGTATGCTTAGCTGCT 1560
DB 1501 CTGATCACTATATCGTTTAACTGTCAATCTCTTCTTTTGTGTATGCTTAGCTGCT 1560
QY 1561 CTAGCATGCTACCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1620
DB 1561 CTAGCATGCTACCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1620
QY 1621 AATAATACCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1662
DB 1621 AATAATACCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1662

RESULT 7
US-08-288-065A-12
; Sequence 12, Application US/08288065A
; Patent No. 5961982
; GENERAL INFORMATION:
; APPLICANT: Cochran, Mark D
; APPLICANT: Macdonald, Richard D
; TITLE OF INVENTION: Recombinant Herpesvirus of Turkeys S-
; NUMBER OF SEQUENCES: 56
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: John P. White
; STREET: 1185 Avenue of the Americas
```

CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/288,065A
FILING DATE: Aug-09-94
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: White, John P
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)278-0400
TELEFAX: (212)391-0526
TELEX: 422523
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 1662 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
FEATURE:
NAME/KEY: CDS
LOCATION: 1..1662
US-08-288-065A-12

Query Match 85.0%; Score 1412.4; DB 2; Length 1662;
Best Local Similarity 90.6%; Pred. No. 0;
Matches 1506; Conservative 0; Mismatches 156; Indels 0; Gaps 0;

QY	1	ATGGGCTCCAGATCTTCTACAGGATCCAGTACCTCTGATGCTCAGCGTCGGGTCCGG	60
DB	1	ATGGGCTCCAGACCTTCTACCAAGAACCCAGACCTATGATGCTCAGTATCCGGGTCCGG	60
QY	61	CTGGCACTGAGTTGGTCTGTCGACAAAGTCCCTTGTATGGCAGCGCTTTCGACGTGCA	120
DB	61	CTGGTACTGAGTTGGTCTGTCGACAAAGTCCCTTGTATGGCAGCGCTTTCGACGTGCA	120
QY	121	GGGATTTGGTGGACAGGAGCAAAAGCAGTCAACATATACCTCTCAGACAGGTC	180
DB	121	GGAAITGGTGGTACAGGAGCAAAAGCAGTCAACATATACCTCTCAGACAGGTC	180
QY	181	ATCATAGTCAAGTTACTCCCAATATGCCCAGGATAAGAGCGGTGTGCAAAAGCCCG	240
DB	181	ATCATAGTTAAGTCTCTCCGAATCTGCCAAGGATAAGGAGGATGTGCGAAGCCCGC	240
QY	241	TTGGAGGGGTACAAAGACGATGACTTGTCTCAGCCCGCTTGGTGAATTTCTTTCGT	300
DB	241	TTGGATGATACAAAGACGATTTGACCTTTTGTCTCAGCCCGCTTGGTGAATTTCTTTCGT	300
QY	301	AGGATACAGAGTCTGTGACTACATCTGGAGGAGGAAACAGGAGCGCTTATAGCGCC	360
DB	301	AGGATACAGAGTCTGTGACTACATCTGGAGGAGGAAACAGGAGCGCTTATAGCGCC	360
QY	361	ATTATCGCGGTGACGCTCTCGGGTGTCAACCGCTGCACAGATAACAGCAGCTTCGGCT	420
DB	361	ATTATCGCGGTGAGCTCTTGGGGTGTCAACCTGGCGGACAAATTAACAGCGCGCAGCT	420
QY	421	CTGATACAGCAACCAAAATGCTGCCACATCTCCGGCTTAAGAGAGATTTCTGCA	480
DB	421	CTGATACAGCAACCAAAATGCTGCCACATCTCCGGCTTAAGAGAGATTTCTGCGCA	480
QY	481	ACCAATGAGGCTGTGCAGAGTCACTGATGATTATCAACATAGCAGTGGCAGTTGGG	540
DB	481	ACCAATGAGGCTGTGCATGAGTCACTGACGATTTATCGCACTAGCAGTGGCAGTTGGG	540

QY	541	AAGATGCAGCAATTTGTTAATGACCAAGTTTAAATAAAGCAGCTCAGAAATTGACTGTATA	600
DB	541	AAGATGCAGCAATTTGTTAATGACCAAGTTTAAATAAAGCAGCTCAGAAATTGACTGTATA	600
QY	601	AAAATTTACCCAGCAGGTTGGTGTAGAACTCAACCTGTATCTAACTGAATTTGACTACAGTA	660
DB	601	AAAATTTGACAGCAAGTTGGTGTAGAGCTCAACCTGTATCTAACTGAATTTGACTACAGTA	660
QY	661	TTGGGCCCCAACAATCATTCCCTGCTTAACCCAGCTGACTATCCAGCGCTTTACAAAT	720
DB	661	TTGGGACCACAAATCATTCCCTGCTTAACCCAGCTGACTATTTACAGCACTTTACAAAT	720
QY	721	CTAGCTGGTGGAAATATGGAATTTACTTTGTTAGTAAAGTTAGGTAGGAAACAACCAATC	780
DB	721	CTAGCTGGTGGAAATATGGAATTTACTTTAGTAAAGTTAGGTAGGAAACAATCAATC	780
QY	781	AGCTCAATTAATTTGGTGGGCTGATACACCGGCAACCTATTTCTGACTCAGACTCAGACT	840
DB	781	AGCTCAATTAATTTGGTGGGCTTAATCACCAGTAACTTCTATACAGCTCAGACTCAGACT	840
QY	841	CAGCTCTTGGGTATACAGGTAACCTACCTCAGTCGGGAACCTGAATAATATGCGTCC	900
DB	841	CAACTCTTGGGTATACAGGTAACCTACCTCAGTCGGGAACCTGAATAATATGCGTCC	900
QY	901	ACCTACTTGGAAACCTTCTGTAGTAAACCAAGGATTTGCTCAGACTCCTGTCCTCA	960
DB	901	ACCTACTTGGAAACCTTATCGTAAACCAAGGATTTGCTCAGACTCCTGTCCTCA	960
QY	961	AAGTGTGTGATGAAGTTCGGTTCGGTATAGAGAACTTGACACTCTCATATCTGTATAGAG	1020
DB	961	AAAGTGTGTGACACGGGTCGGTTCGGTATAGAGAACTTGACACTCTCATATCTGTATAGAG	1020
QY	1021	ACCGATTTGGATCTATATTTGACAGATAGTGCATCTCCCTATCTCTCTCTCTCTCTCT	1080
DB	1021	ACTGACTTAGATTTATATTTGACAGATAGTGCATCTCCCTATCTCTCTCTCTCTCTCT	1080
QY	1081	TCCTGTTTGGCGGCAATACATCGCTTTCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	1140
DB	1081	TCCTGTTTGGCGGCAATACATCGCTTTCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	1140
QY	1141	AGCGGTACATGACTCTCAAGGCTCAGTTATTTGCTCAACTGTATAGATGACAACTGTAGA	1200
DB	1141	ACACCATATATGACTATCAAGGCTCAGTCTATCGTAACTGCAAGATGACAACTGTAGA	1200
QY	1201	TGTCAGACCCCGGGTATCATATCGCAAAATTTGAGAGGCTGCTCTCTCTCTCTCTCTCT	1260
DB	1201	TGTTGAAACCCCGGGTATCATATCGCAAAATTTGAGAGGCTGCTCTCTCTCTCTCTCTCT	1260
QY	1261	AGGCAATCATGCAATGTCTCTATCTCTTACAGGAAATACCTTTGAGGCTCAGTGGGAAATTT	1320
DB	1261	AAACCAATCATGCAATGTCTCTATCTCTTACAGGAAATACCTTTGAGGCTCAGTGGGAAATTT	1320
QY	1321	GATGCACTTATCAAAAGATATCTCAATACAGATTTCTCAAGTATCTGTCAGCAGGCAAT	1380
DB	1321	GATGTAATCTTATCAAGAGATATCTCAATACAGATTTCTCAAGTATTAATAACAGGCAAT	1380
QY	1381	CTCGATATCTCGACTGAGCTTTGGGAATGTCAACAACTCGATAAGTAATGCTTTAGATAAG	1440
DB	1381	CTTGATATCTCACTGAGCTTTGGGAATGTCAACAACTCGATGATGATGCTTTAGATAAG	1440
QY	1441	TTAGAGGAAACCAACAGCAAACTAGACAAAGTCAATGTCAAACTGACAGCAATCCCGT	1500
DB	1441	TTAGAGGAAACCAACAGCAAACTAGACAAAGTCAATGTCAAACTGACAGCAATCCCGT	1500
QY	1501	CTCATCCTATATCTGTTTAACTGTCATATCTCTGTTTGGTGTACTTAGCTGGT	1560
DB	1501	CTCATCCTATATCTGTTTAACTGTCATATCTCTGTTTGGTGTACTTAGCTGGT	1560
QY	1561	CTAGCATGCTACCTGATGTACAAGCAAAAGGCGCAACAAGACCTTTGTTGCTTGGG	1620
DB	1561	CTAGCATGCTACCTAAATGTACAAGCAAAAGGCGCAACAAGACCTTTATTTGCTTGGG	1620
QY	1621	AATAATACCTTGGATCAGATGAGAGCCACTAGAGAAATGTGA	1662

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1621 AATAATACCTAGATCAGATGAGAGCCACTACAAAAATGTGA 1662

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RESULT 8
US-08-362-240A-12
; Sequence 12, Application US/08362240A
; Patent No. 5965138
; GENERAL INFORMATION:
; APPLICANT: Cochran, Mark D
; APPLICANT: Junker, David
; APPLICANT: Wild, Martha A
; TITLE OF INVENTION: Recombinant Herpesvirus and Uses Thereof
; NUMBER OF SEQUENCES: 60
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: John P. White
; STREET: 1185 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/362,240A
; FILING DATE: Dec-22-94
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: White, John P
; REGISTRATION NUMBER: 28,678
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212)278-0400
; TELEFAX: (212)391-0526
; TELEX: 422523
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1662 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..1662
US-08-362-240A-12

Query Match 85.0%; Score 1412.4; DB 2; Length 1662;
Best Local Similarity 90.6%; Pred. No. 0;
Matches 1506; Conservative 0; Mismatches 156; Indels 0; Gaps 0;

QY 1 ATGGGCTCCAGATCTTCTACAGAGTCCAGTACCTTGATGCTGACCGTCCGGTCCGG 60
Db |||||
QY 1 ATGGGCTCCAGATCTTCTACAGAGTCCAGTACCTTGATGCTGACCGTCCGGTCCGG 60
Db |||||
QY 61 CTGGCACTGATGTTGGCTCTGCGCAAGCTCCCTTGATGGCAGGCTCTTGCGAGCTGCA 120
Db |||||
QY 61 CTGGTACTGATGTTGGCTCTGCGCAAGCTCCCTTGATGGCAGGCTCTTGCGAGCTGCA 120
Db |||||
QY 121 GGGATTGTGTGACAGAGACAAAGCAGTCAACATATACATACACCTCATCTCAGACAGGTC 180
Db |||||
QY 121 GGAATTGTGTGACAGAGACAAAGCAGTCAACATATACATACACCTCATCTCAGACAGGTC 180
Db |||||
QY 181 ATCATAGTCAAGTTACTCCCAATATGCCCAAGATAAAGAGGCTGTGCAAAAGCCCG 240
Db |||||
QY 181 ATCATAGTTAAGTCTCTCCCAATATGCCCAAGATAAAGAGGCTGTGCAAAAGCCCG 240
Db |||||
QY 241 TTGGAGCGGTACACAGGACATTGACTACTTGTCTACCCCTTGGTGTGATTCTATTTCGT 300
Db |||||
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1381 CTCGATATCTCGACTGAGCTTGGGAATGTCACAACTCGATAGTAAGTCTTAGATAAG 1440
1381 CTTGATATCTCAACTGAGCTTGGGAATGTCACAACTCGATAGTAAGTCTTAGATAAG 1440
1441 TTAGAGGAAGCAACAGCAAACTAGACAAAGTCAATGTCAAACTGACACGACATCCGCT 1500
1441 TTAGAGGAAGCAACAGCAAACTAGACAAAGTCAATGTCAAACTGACACGACATCCGCT 1500
1501 CTCATCAGCTATATCGTTTAACTGTCTATCTCTTGTGTTGTTGTTGTTGTTGTTGTT 1560
1501 CTCATCAGCTATATCGTTTAACTGTCTATCTCTTGTGTTGTTGTTGTTGTTGTTGTT 1560
1561 CTAGCATCTACCTGATGTACAAAGCAAAAGGCGCAACAGAGACCTCTTATGTTGTTGG 1620
1561 CTAGCATCTACCTGATGTACAAAGCAAAAGGCGCAACAGAGACCTCTTATGTTGTTGG 1620
1621 AATTAATCCCTGGATCAGATGAGAGCCACTAGAAAATGTGA 1662
1621 AATAATACCTTAGATCAGATGAGAGCCACTACAAAATGTGA 1662

RESULT 9

US-08-804-372A-10
; Sequence 10, Application US/08804372A
; Patent No. 6183753
; GENERAL INFORMATION:
; APPLICANT: Cochran, Mark D.
; APPLICANT: Wild, Martha A.
; APPLICANT: Winslow, Barbara J.
; TITLE OF INVENTION: Recombinant Chimeric Viruses and Uses
; TITLE OF INVENTION: Thereof
; NUMBER OF SEQUENCES: 32
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooper & Dunham LLP
; STREET: 1185 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/804,372A
; FILING DATE:
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: White, John P.
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 2552/39115E
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 278-0400
; TELEFAX: (212) 391-0525
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1662 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..1662

US-08-804-372A-10

Query Match 85.0%; Score 1412.4; DB 3; Length 1662;
Best Local Similarity 90.6%; Pred. No. 0;
Matches 1506; Conservative 0; Mismatches 156; Indels 0; Gaps 0;

QY 1 ATGGGCTCCAGATCTTCTACAGGATCCAGTACTCTGATGCTGACCGTCCGGTCCGG 60
DB 1 ATGGGCTCCAGATCTTCTACCAAGAACCCAGCACTATGATGCTGACTATCCGGTCCGG 60
QY 61 CTGGCAGTCTAGTCTGCTGCTCCGACAAAGCTCCCTTGTATGTCAGAGCCCTCTTGCAGCTGCA 120
DB 61 CTGGTACTGAGTCTGCTGCTCCGGCAAACTCCATGATGAGAGCCCTCTTGCAGCTGCA 120
QY 121 GGGATTGTGGTGA CAGGAGACAAAGAGCTCAACATATACACCTCATCTCAGACAGGTCAT 180
DB 121 GGAATTTGGTGTACAGGAGACAAAGAGCTCAACATATACACCTCATCTCAGACAGGTCAT 180
QY 181 ATCATAGTCAAGTTACTCCCAATATGCCCAGAAAGTAAAGAGGCGTGTGCAAAAGCCCGG 240
DB 181 ATCATAGTTAAGTCTCTCCCAATATGCCCAGAAAGTAAAGAGGCGTGTGCAAAAGCCCGG 240
QY 241 TTGAGGCGTCAACAGAGACATTTGACTACTTTTGTCTCACCCCTTTGGTGTATTTATTCGT 300
DB 241 TTGGATGCATACAAACAGAGACATTTGACTACTTTTGTCTCACCCCTTTGGTGTATTTATTCGT 300
QY 301 AGGATACAGAGTCTGTGATCTACATCTGGAGAGGGGAAACAGGAGACGCTTTATAGGCGCC 360
DB 301 AGGATACAGAGTCTGTGACTACATCTGGAGAGGGGAGACAGGAGCGCTTTATAGGCGCC 360
QY 361 ATTATCGCGGTGCAGCTCTCGGGGTTGCAACCGCTGCACAGATAACAGAGAGCTTCGGCT 420
DB 361 ATTATCGCGGTGTGGCTCTTGGGGTTGCAACTCGCGGCAAAATAACAGCGCGCGAGCT 420
QY 421 CTGATACAAGCCAAACAAATGCTGCCAAACATCTCGGGCTTAAAGAGAGAAATGCTGCA 480
DB 421 CTGATACAAGCCAAACAAATGCTGCCAAACATCTCGGGCTTAAAGAGAGCAATGCGGCA 480
QY 481 ACCAATGAGCTGTGCAGAGGTCACATGATGATATTCACAACTAGCAGTGGCAGTTGGG 540
DB 481 ACCAATGAGGCTGTGCATGAGGTCACATGAGCGGATTTATCGCAACTAGCAGTGGCAGTTGGG 540
QY 541 AAGATGAGCAATTTGTTTAAAGACAGTTTAAATAAAGCAGCTCAGGAATTCGACTGTATA 600
DB 541 AAGATGAGCAGTTCTGTTTAAAGACCAATTTAAATAAAGCAGCTCAGGAATTTAGCTGCA 600
QY 601 AAAATTATCCAGCAGGTTGGTGTAGAACTCAACCTGTATCTAAGTAAATGACTACAGTA 660
DB 601 AAAATTGACAGCAAGTTGGTGTAGAGCTCAACCTGTACCTAACCGAATCGACTACAGTA 660
QY 661 TTGGGGCCACAAATCAGTTCCCTTAAACCGAGCTGACTATCCAGGCGCTTTACAA 720
DB 661 TTGGGACCAAAATCAGTTCCCTTAAACAGGCTGACTATTCAGGCACTTTTACAA 720
QY 721 CTAGCTGGTGGGAATATGGATTACTTGTGACTAAGTTAGGTGAGGGAACAAACCACTC 780
DB 721 CTAGCTGGTGGGAATATGGATTACTTGTGACTAAGTTAGGTGAGGGAACCAATCACTC 780
QY 781 AGCTCATTAATTTGGTAGCGGCTGATCACCGGCAACCTATTTCTGTAGCAGTCAAGACT 840
DB 781 AGCTCATTAATTCGGTAGCGGCTTAATCACCGGTAACCTATTTCTATACGACTCAGACT 840
QY 841 CAGCTCTGGGTATACAGGTAAACCTTACCTCCCTCAGTCCGGGACCTGATATATCGTGCC 900
DB 841 CAATCTTGGGTATACAGGTAACTCTACCTTTCAGTCCGGGAACCTTAAATAATATCGTGCC 900
QY 901 ACCTACTTGGAAACCTTGTCTGTAAAGTACAAACAAAGGATTTGCTCAGCACTCGTCCCA 960
DB 901 ACCTACTTGGAAACCTTATCCGTAAGACAAACAGGAGGATTTGCTCAGCACTGTGCCA 960
QY 961 AAGTGTGTGATGAGGTCGGTTCGGTGTATAGAGAACTTGCACCTCATCTGTATAGAG 1020
DB 961 AAGTGTGTGACACGGGTCGGTTCGTGTATAGAGAACTTGCACCTCATCTGTATAGAA 1020
QY 1021 ACCGATTTGGATCTATATTTGTACAGAAATAGTGACATTTCCCTATGTCTCTCGGTATTTAT 1080
DB 1021 ACTGACTTAGATTTATATTTGTACAGAAATAGTAGTTCCCTATGTCCCTTGGTATTTTAC 1080

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QY 1081 TCCTGTTGAGCGGCAATACATCGGCTTGCATGTACTCGAAGACTGAAGCGCACTCACT 1140
D 1081 TCCTGTTGAGCGGCAATACATCGGCTTGCATGTACTCGAAGACTGAAGCGGCACTCACT 1140
QY 1141 AGCCCGTACATGACTCTCAAGGCTCAGTTATTGCCAAGTGAAGATGACAACTAGTA 1200
D 1141 ACACCATATGACTATCAAGGCTCAGTCATCGCTAATGCAAGATGACAACTAGTA 1200
QY 1201 TGTGAGAGCCCCCGGTTATCATATCGAAAAATATGAGAGAGCTGTCTCTTAATAGAT 1260
D 1201 TGTGTAAGCCCCCGGTTATCATATCGAAAAATATGAGAGAGCTGTCTCTTAATAGAT 1260
QY 1261 AGGCATCATGCAATGCTCTATCTCTTAGACGGAATACCTTTGAGGCTCAGTGGGAATTT 1320
D 1261 AAACAATCATGCAATGCTCTATCTCTTAGGCGGATACCTTTAAGGCTCAGTGGGAATTC 1320
QY 1321 GATGCAACTTATCAAAAGAAATATCTCAATACAAAGATTCTCAAGTAATCGTGACAGGCAAT 1380
D 1321 GATGTAATCATCAAGAAATATCTCAATACAAAGATTCTCAAGTAATCAATACAGGCAAT 1380
QY 1381 CTCGATATCTCGACTGAGCTTGGGAATGCAACAACTCGAATAGTAATGCTTTAGATAAG 1440
D 1381 CTTGATATCTCAACTGAGCTTGGGAATGCAACAACTCGATCAGTAATGCTTTGAATAAG 1440
QY 1441 TTAGAGGAAGCAACAGCAAACTAGACAAAGTCAATGTCAAACTGACGACCATCGCT 1500
D 1441 TTAGAGGAAGCAACAGCAAACTAGACAAAGTCAATGTCAAACTGACGACCATCGCT 1500
QY 1501 CTCATCACCTATATCTGTTTAACTGTCAATATCTCTTGTGTTTGTGTTATCTTAGCCCTGGTT 1560
D 1501 CTCATTAACCTATATCTGTTTAACTGTCAATATCTCTTGTGTTTGTGTTATCTTAGCCCTGGTT 1560
QY 1561 CTAGCATGCTACGTATGTAACAGCAAAAGCGCAACAGAAAGCTTTGTTATGCTTTGGG 1620
D 1561 CTAGCATGCTACGTATGTAACAGCAAAAGCGCAACAGAAAGCTTTGTTATGCTTTGGG 1620
QY 1621 AATAATACCTGATCAGATGAGAGCCACTACGAAATGTGA 1662
D 1621 AATAATACCTGATCAGATGAGAGCCACTACGAAATGTGA 1662
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RESULT 10

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PCT-US95-10245-12
; Sequence 12, Application PC/TUS9510245
; GENERAL INFORMATION:
; APPLICANT: SYNTRO CORPORATION
; TITLE OF INVENTION: Recombinant Herpesvirus of Turkeys And Uses Thereof
; NUMBER OF SEQUENCES: 60
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: John P. White
; STREET: 1185 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/10245
; FILING DATE: 09-AUG-1995
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: White, John P
; REGISTRATION NUMBER: 28,678
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212)278-0400
; TELEFAX: (212)391-0526
; TELEX: 422523
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
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; LENGTH: 1662 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..1662
; PCT-US95-10245-12

Query Match      85.0%; Score 1412.4; DB 5; Length 1662;
Best Local Similarity 90.6%; Pred. No. 0;
Matches 1506; Conservative 0; Mismatches 156; Indels 0; Gaps 0;

QY 1 ATGGGCTCCAGATCTTTCTACAGGATCCAGACTACCTCTGATGCTACCGTCCGGGTGCGG 60
D 1 ATGGGCTCCAGATCTTTCTACAGGATCCAGACTACCTCTGATGCTACCGTCCGGGTGCGG 60
QY 61 CTGGCACTGAGTTGGTCTGTCCGCAAGCTCCCTTGTATGGCAGGCTCTTGCAGTCA 120
D 61 CTGGTACTGAGTTGGTCTGTCCGCAAGCTCCCTTGTATGGCAGGCTCTTGCAGTCA 120
QY 121 GGGATTGTGTCAGAGGAGACAAAGCAGTCAACATATACACCTCATCTCAGACAGGTCA 180
D 121 GGAATTGTGTTACAGGAGACAAAGCAGTCAACATATACACCTCATCTCAGACAGGTCA 180
QY 181 ATCATAGTCAAGTTACTCCCAATATGCCCCAAGATAAAGAGCGGTGTGCAAAAGCCCCG 240
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D 241 TTGGATGTCATACAAACAGGACATTTGCTCACCCTTGGTGAATCTTATTCGT 300
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D 301 AGGATACAAAGTCTGTGACTACATCTGAGAGGAGAGAGAGGAGCGCTTATAGCGGC 360
QY 361 ATTATCGGCGGTGACGCTCTCGGGGTGCAACCGCTGTCAGAGATAACAGCAGCTTCGGCT 420
D 361 ATTATTTGGCGGTGTGGCTCTTGGGGTTGCACTGCGGCAAAATAACAGCGCGCGAGCT 420
QY 421 CTGATACAAAGCCAAACAAATGCTGCAACATCTCGGCTTAAAGAGAGAAATGTGCA 480
D 421 CTGATACAAAGCCAAACAAATGCTGCAACATCTCGGCTTAAAGAGAGAAATGTGCA 480
QY 481 ACCAATGAGGCTGTGACAGGAGTCACTGATGATATATCAAACTAGCAGTGGCAGTTGGG 540
D 481 ACCAATGAGGCTGTGATGAGTCACTGCGGATATCGCAATTCGCACTAGCAGTGGG 540
QY 541 AAGATCAGCAATTTGTTAATGACCAAGTTAATAAAGAGCTCAGGAATGGACTGTATA 600
D 541 AAGATCAGCAGTTGCTTAAATGACCAATTTAATAAAGAGCTCAGGAATGGACTGTATA 600
QY 601 AATAATCCAGCAGGTTGTTGATAGTCAACCTGTATCTAATCTAAGTGAAGTCAAGTA 660
D 601 AATAATCCAGCAGGTTGTTGATAGTCAACCTGTATCTAATCTAAGTGAAGTCAAGTA 660
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D 661 TTGGGCGCAAAATCACTTCCCTGCTTAAACCCAGTCACTATCAGGCGCTTTTCAAT 720
QY 721 CTAGCTGGTGGGAATATGGAATTTGTTGACTTAAGTTAGGTAGGGAACCAACCACTC 780
D 721 CTAGCTGGTGGGAATATGGAATTTGTTGACTTAAGTTAGGTAGGGAACCAACCACTC 780
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D 781 AGCTCATTAATTTGGTAGCGGCTGTATCAGGCAACCTTATCTGTACGACTCAGAGCT 840
QY 841 CAGCTCTTGGGTATACAGGTTAACCTTACCTCAGTCGGGAACCTGAATAATATATGCGTGC 900
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Db 841 CAACCTCTGGGTATACAGTAACCTCTACCTTCAGTCGGGAACCTAAATAATATGCTGCC 900
Qy 901 ACCTACTTGGAAACCTCTCTGTAGTACACCAAGGATTTGCCCTCAGACTCGTCCCA 960
Db 901 ACCTACTTGGAAACCTCTCTGTAGTACACCAAGGATTTGCCCTCAGACTCGTCCCA 960
Qy 961 AAGGTGCTGATGAAGTTCGGTTCCTGTATAGAGAACTTGACACCTCATCTGTATAGAG 1020
Db 961 AAGGTGCTGATGAAGTTCGGTTCCTGTATAGAGAACTTGACACCTCATCTGTATAGAG 1020
Qy 1021 ACCGATTTGGATCTATATTTGTAAGAAATAGTACATTTCCCTATGCTCTCCCTGATTTAT 1080
Db 1021 ACTGACTTAGATTTATATTTGTAAGAAATAGTACATTTCCCTATGCTCTCCCTGATTTAT 1080
Qy 1081 TCCTGTTTGGGGCAATACATCGCTTCGCTGATGTAAGTCTGAGACTGAAGGGCACTACT 1140
Db 1081 TCCTGCTTGGGGCAATACATCGCTTCGCTGATGTAAGTCTGAGACTGAAGGGCACTACT 1140
Qy 1141 ACGCGGTACATGACTCTCAAGGGCTCAGTTATTTGCAACTGTGAAGTACACACATGTAGA 1200
Db 1141 ACACATATATGACTATCAAGGGCTCAGTCTGCTAATCTGCAAGTACACACATGTAGA 1200
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Db 1201 TGTGTAACCCCGGGTATCATATCGCAAAATTTATGGAAGTCTGCTCTAATAGAT 1260
Qy 1261 AGGCAATCATGATGCTCTATCTCTAGACGGAATATTTGAGGCTCAGTGGGGAATTT 1320
Db 1261 AAACAATCATGATGTTTATCTCTTAGCGGGATTAATTTAAGGCTCAGTGGGGAATTC 1320
Qy 1321 GATGCAACTTATCAAAAATATCTCAATACAAAGATTTCTCAAGTAATCGTGACAGGCAAT 1380
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Qy 1381 CTCGATATCTGATGACTTGGGAATGCAAACTCTCAAGTCTGATGATGCTTTAGATAAG 1440
Db 1381 CTTGATATCTCAACTGACTTGGGAATGCAAACTCTCAAGTCTGATGATGCTTTAGATAAG 1440
Qy 1441 TTAGAGGAAGCAACAGCAACTAGCAAGTCTCAAGTCTCAAGTCTCAAGTCTCAAGTCT 1500
Db 1441 TTAGAGGAAGCAACAGCAACTAGCAAGTCTCAAGTCTCAAGTCTCAAGTCTCAAGTCT 1500
Qy 1501 CTCATCACTATATCGTTTAACTGTCATATCTCTGTTTGGTATGATGCTTGGCTGTT 1560
Db 1501 CTCATTAACCTATATCGTTTAACTGTCATATCTCTGTTTGGTATGATGCTTGGCTGTT 1560
Qy 1561 CTAGATGCTTACCTGATGTAAGCAAGCAAGGCGCAACAGAGACCTTGTATGCTTGGG 1620
Db 1561 CTAGATGCTTACCTGATGTAAGCAAGCAAGGCGCAACAGAGACCTTGTATGCTTGGG 1620
Qy 1621 AATAATACCTTGGATCAGATGAGAGCCACTACGAAATGTGA 1662
Db 1621 AATAATACCTTGGATCAGATGAGAGCCACTACGAAATGTGA 1662
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RESULT 11

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US-08-484-575A-12
Sequence 12, Application US/08484575A
Patent No. 5926358
GENERAL INFORMATION:
APPLICANT: Mark D. Cochran and David E. Junker
TITLE OF INVENTION: Recombinant Fowlpox Viruses and Uses Thereof
NUMBER OF SEQUENCES: 42
CORRESPONDENCE ADDRESS:
ADDRESSEE: John P. White
STREET: 1185 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/484,575A
FILING DATE: 07-JUN-1995
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: White Esq, John P
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)278-0450
TELEFAX: (212)391-0525
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 4177 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
FEATURE:
NAME/KEY: CDS
LOCATION: 115..1860
FEATURE:
NAME/KEY: CDS
LOCATION: 2095..3756
US-08-484-575A-12
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Query Match 85.0%; Score 1412.4; DB 2; Length 4177;
Best Local Similarity 90.6%; Pred. No. 0;
Matches 1506; Conservative 0; Mismatches 156; Indels 0; Gaps 0;

Qy 1 ATGGGCTCCAGATCTTCTACAGGATCCAGTACCTGTGATGCTGACCGTCCGGTCCGC 60
Db 2095 ATGGGCTCCAGATCTTCTACAGGATCCAGTACCTGTGATGCTGACCGTCCGGTCCGC 2154
Qy 61 CTGGCACTGAGTTCGGTCTGTCCGACAGCTCCCTGTGATGCGAGCCCTTTGCACTGCA 120
Db 2155 CTGGTACTGAGTTCGATCTGTCCGCAAACTCCATTTGATGCGAGCCCTTTGCACTGCA 2214
Qy 121 GGGATTGTGTGACAGGAGCAAAAGCAGTCAACATATACACCTCATCTCAGACAGGGTCA 180
Db 2215 GGAATTGTGTTACAGGAGCAAAAGCAGTCAACATATACACCTCATCTCAGACAGGGTCA 2274
Qy 181 ATCATAGTCAAGTTACTCCCAATATATGCCCAAGATTAAGAGGCGTGTGCAAAAGCCCGC 240
Db 2275 ATCATAGTCAAGTCTCTCCGAAATCTGCCAAAGGATTAAGAGGCGTGTGCAAAAGCCCGC 2334
Qy 241 TTGGAGGCGTACAAACAGGACATTTGACTACTTTGCTCACCCTTGTGCTGATTTCTTTCGT 300
Db 2335 TTGGATGCTATCAACAGGACATTTGACCACTTTGCTCACCCTTGTGCTGATTTCTTTCGT 2394
Qy 301 AGGATACAAGAGTCTGTGACTACATCTGAGAGGGGAAACAGGAGCCCTTTATAGGGGCC 360
Db 2395 AGGATACAAGAGTCTGTGACTACATCTGAGAGGGGAAACAGGAGCCCTTTATAGGGGCC 2454
Qy 361 ATTATCGGCGTGCAGCTCTCGGGTTGCAACCGCTGCAAGATTAACAGAGCTTTCGGCT 420
Db 2455 ATTATCGGCGTGTGGCTCTTTGGGGTTGCAACTCTGCCGCAAAATTAACAGAGCGCGAGCT 2514
Qy 421 CTGATACAAGCCAAACCAAAATGCTGCCAATCTCTCGGCTTTAAAGAGAGAAATTTGCTGCA 480
Db 2515 CTGATACAAGCCAAACCAAAATGCTGCCAATCTCTCGGCTTTAAAGAGAGAAATTTGCTGCA 2574
Qy 481 ACCAATGAGGCTGTGACAGAGTCACTGATGATGATTTACAACTAGCAGTGGCAGTTGGG 540
Db 2575 ACCAATGAGGCTGTGATGAGTCACTGACCGATTTATCGCAACTAGCAGTGGCAGTTGGG 2634
Qy 541 AAGATGAGCAATTTGTTATGACAGTTTAAATAAACAGCTCAGGAATTTGAGCTGTATA 600
Db 2635 AAGATGAGCAGTTTCGTTAATGACCAATTTAATAAACAGCTCAGGAATTTAGACTGTATC 2694
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QY 601 AAAAAATACCCAGCAGGTTGGTGTAGAACTCAACCTGTATCTAACTGAATGACTACAGTA 660
Db 2695 AAAAAATGCAAGCAAGTGGTGTAGAGCTCAACCTGTACCTAACCGAATCGACTACAGTA 2754
QY 661 TTCGGGCCCCAAATCACTTCCCTCCCTGCTTAAACCCAGCTGACTATCCAGGGCGTTTCAAT 720
Db 2755 TTCGGGACCACAAATCACTTCCCTGCTTAAACCCAGCTGACTATCCAGGGCGTTTCAAT 2814
QY 721 CTAGCTGGTGGGAATATGGAATTAATCTTGTGCTAAGTATAGGTAGGTAGGAAACAACCAATC 780
Db 2815 CTAGCTGGTGGGAATATGGAATTAATCTTGTGCTAAGTATAGGTAGGTAGGAAACAATCAATC 2874
QY 781 AGCTCATTAATGGTAGCGGCTGATCACCGGCAACCCATTCTGTAGCACTCACAGCT 840
Db 2875 AGCTCATTAATGGTAGCGGCTTAAATCACCGGTAACCCCTATTCTATACGACTCACAGCT 2934
QY 841 CAGCTCTTGGGTATACAGGTAACCCCTACCTCCAGTCCGGGAACCTGAATATATGCGGTGCC 900
Db 2935 CAACTCTTGGGTATACAGGTAACCTTACCTTCAGTCGGGAACCTGAATATATGCGGTGCC 2994
QY 901 ACCTACTTGGAAACCTTGTCTGAAGTAACAACCAAGGATTTGCTCAGCACTCGTCCCA 960
Db 2995 ACCTACTTGGAAACCTTATCCGTAAGCACCAACGAGGGATTTGCTCAGCACTGTCCCA 3054
QY 961 AAGGTGGTATGAAGGTTCGGTTCGGTGATAGAGAACTTCACACCTCATACTGTATAGAG 1020
Db 3055 AAGGTGGTATGAAGGTTCGGTTCGGTGATAGAGAACTTCACACCTCATACTGTATAGAA 3114
QY 1021 ACCGATTTGGATCTATATTGTACAAGAAATAGTGACATTCCTCTATGCTCTGGTATTAT 1080
Db 3115 ACTGACTTAGATTTATTTGTACAAGAAATAGTAGGTTCCCTATGCTCCCTGGTATTAC 3174
QY 1081 TCCTGTTTGGCGGCAATACATCGGCTTGCATGTACTCGAAGACTGAAGCGGCACTACT 1140
Db 3175 TCCTGTTTGGCGGCAATACATCGGCTTGCATGTACTCGAAGACTGAAGCGGCACTACT 3234
QY 1141 ACCGCTGATGACTCTCAAGGCTCAGTTATTCGCAACTGTAAGTGAACAATGATAGA 1200
Db 3235 ACACATATATGACTCAAGGCTCAGTATCGCTAACTGCAAGATGACAATGATAGA 3294
QY 1201 TGTGCAGACCCCGGGTATCATATCGCAAAATATGGAAGCTGTGTCTCTAATAGAT 1260
Db 3295 TGTGTAACCCCGGGTATCATATCGCAAAATATGGAAGCTGTGTCTCTAATAGAT 3354
QY 1261 AGCAATATGCAATGCTCTATCTCTAGACGGAATTAATTTGAGGCTCAGTGGGGAATTT 1320
Db 3355 AAACAATCATGCAATGTTTATCTTGGCGGGATTAATTTAAGGCTCAGTGGGGAATTT 3414
QY 1321 GATGCAACTTATCAAAAGAAATATCTCAATACAGATTTCTCAAGTAATCGTGACAGGCAAT 1380
Db 3415 GATGCAACTTATCAAAAGAAATATCTCAATACAGATTTCTCAAGTAATTAATTAAGGCAAT 3474
QY 1381 CTCGATATCTCGACTGAGCTTGGGAATGTCAACAACTCGATAAGTAAATGCTTTAGATAAG 1440
Db 3475 CTTGATATCTCAACTGAGCTTGGGAATGTCAACAACTCGATAGTAATGCTTTGAAATAG 3534
QY 1441 TTAGAGAAAGCAACAGCAATAGACAAGGTCAAAGTCAAACTGACAGCAATCGGCT 1500
Db 3535 TTAGAGAAAGCAACAGCAATAGACAAGGTCAAAGTCAAACTGACAGCAATCGGCT 3594
QY 1501 CTCATCACCTATATCGTTTAACTGTATATCTCTGTTGTTGTTGTTGTTGTTGTTGTT 1560
Db 3595 CTCATCACCTATATCGTTTAACTGTATATCTCTGTTGTTGTTGTTGTTGTTGTTGTT 3654
QY 1561 CTAGCATGCTACCTGTATGTAAGCAAAAGCGCAACAGAAAGACCTTGTATGCTTGGG 1620
Db 3655 CTAGCATGCTACCTGTATGTAAGCAAAAGCGCAACAGAAAGACCTTGTATGCTTGGG 3714
QY 1621 AATAATACCTTGATGATGAGGCACTACGAAATGTGA 1662
Db 3715 AATAATACCTTGATGATGAGGCACTACGAAATGTGA 3756

RESULT 12

US-08-477-459-12
; Sequence 12, Application US/08477459
; Patent No. 6001369
; GENERAL INFORMATION:
; APPLICANT: Mark D. Cochran
; TITLE OF INVENTION: Recombinant Fowlpox Viruses and Uses
; TITLE OF INVENTION: Thereof
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: John P. White
; STREET: 1185 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/477,459
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: White Esq, John P
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 278-0400
; TELEFAX: (212) 391-0525
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4177 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHEetical: NO
; ANTI-SENSE: NO
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 115..1860
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 2095..3756
; US-08-477-459-12

Query Match 85.0%; Score 1412.4; DB 3; Length 4177;
Best Local Similarity 90.8%; Pred. No. 0;
Matches 1506; Conservative 0; Mismatches 156; Indels 0; Gaps 0;
QY 1 ATGGGCTCCAGATCTTCTACAGGATCCAGTACCTCTGATGCTGACCGTCCGGGTGCG 60
Db 2095 ATGGGCTCCAGATCTTCTACAGGATCCAGTACCTCTGATGCTGACCGTCCGGGTGCG 2154
QY 61 CTGGCACTGATGTCCTGTCGCAAGCTCCCTTGATGGCAGGCTCTTGACGTGCA 120
Db 2155 CTGGCACTGATGTCCTGTCGCAAGCTCCCTTGATGGCAGGCTCTTGACGTGCA 2214
QY 121 GGGATTTGTGTGACAGGACAAAGCAGTCAACATATACACCTCATCTCAGACAGGTCA 180
Db 2215 GGGATTTGTGTGACAGGACAAAGCAGTCAACATATACACCTCATCTCAGACAGGTCA 2274
QY 181 ATCATAGTCAAGTTACTCCCAATATGCCCCAAGATAAGAGCGGTGTGCAAAAGCCCCG 240
Db 2275 ATCATAGTTAAGTCTCTCCGAATCTGCCAAGATAAGAGCGCATGTGCAAAAGCCCC 2334
QY 241 TTGGAGCGGTACAAAGCAATGACTACTTGTCTACCCCTTGGTGTATCTATCGT 300
Db 2335 TTGGATGTCATACAAAGCAATGACTACTTGTCTACCCCTTGGTGTATCTATCGT 2394
QY 301 AGGATACAAAGTCTGTGACTACATCTGGAGGAGGGAACAGGAGCGCTTATAGCGCC 360

2395 AGGATCAAGAGTCTGTGACTACATCTGGAGGGGGAGACAGGGCGCGCTTTATAGGCGCC 2454
361 ATTATCGCGGTGACAGCTCTCGGGTTGCAACCGCTGCACAGATGAACAGAGCTTTCGGCT 420
2455 ATTATTCGGGTGTGGCTCTTTGGGGTTGCAACCGCTGCACAGATGAACAGAGCTTTCGGCT 2514
421 CTGATACAGGCAACCAAAATGCTGCCAAATCTCTCCGGCTTTAAAGAGAGAAATGCTGCA 480
2515 CTGATACAGGCAACCAAAATGCTGCCAAATCTCTCCGGCTTTAAAGAGAGAAATGCTGCA 2574
481 ACCAATGAGGTGTGCACGAGTCACTGATGATTTATCAAACTAGCAGTGGCAGTTGGG 540
2575 ACCAATGAGGTGTGCATGAGTCACTGACGAGTTATTCGCAACTAGCAGTGGCAGTTGGG 2634
541 AAGATGACGAAATTTGTTAATGACCAAGTTTAAATAAAGAGCTCAGGAATTCGAGTGTATA 600
2635 AAGATGACGAAATTTGTTAATGACCAAGTTTAAATAAAGAGCTCAGGAATTCGAGTGTATA 2694
601 AAAATTACCCAGCAGGTTGGTGTAGAACTCAACCTGTATCTAACTGAATTCAGTACAGTA 660
2695 AAAATTGACAGCAGGTTGGTGTAGAGCTCAACCTGTATCTAACTGAATTCAGTACAGTA 2754
661 TTCGGGCCAATAATCACTTCGCCCTGCTTAACCCAGCTGACTATCCAGCGCCTTTACAA 720
2755 TTCGGGCCAATAATCACTTCGCCCTGCTTAACCCAGCTGACTATTCAGCGCCTTTACAA 2814
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2815 CTAGCTGTGGGAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2874
781 AGCTCATTAATTTGGTGTAGGCGGCTGATCACCGGCAACCTTCTGTAGACTTCACAGACT 840
2875 AGCTCATTAATTTGGTGTAGGCGGCTTAACTACCGGTAACCTTCTGTAGACTTCACAGACT 2934
841 CAGCTCTTTGGGTATACAGGTAACCTTACCTGAGTGGGAACCTGGAATTAATGAGTGGCC 900
2935 CAACCTCTTTGGGTATACAGGTAACCTTACCTGAGTGGGAACCTGGAATTAATGAGTGGCC 2994
901 ACCTACTTTGGAACCTTCTGTAAGTACACCAAGGATTTGCTCAGCACTCGTCCCA 960
2995 ACCTACTTTGGAACCTTCTGTAAGTACACCAAGGATTTGCTCAGCACTCGTCCCA 3054
961 AAGGTGTGTATGAAGTGTGGTTCGGTGTATAGAGAACTTGACACCTCATCTGTATAGAG 1020
3055 AAGGTGTGTATGAAGTGTGGTTCGGTGTATAGAGAACTTGACACCTCATCTGTATAGAG 3114
1021 ACCGATTTGGATCTATATTGTACAAAGATAGTACATTCCTTATGCTCTCTGGTATTTAT 1080
3115 ACTGACTTAGATTTATATTGTACAAAGATAGTACATTCCTTATGCTCTCTGGTATTTAT 3174
1081 TCCTGTTTGGCGGCAATACATCGGCTTGTGATGTAAGAACTTGACACCTCATCTGTATAGAG 1140
3175 TCCTGTTTGGCGGCAATACATCGGCTTGTGATGTAAGAACTTGACACCTCATCTGTATAGAG 3234
1141 ACGCGGTATGACTCTCAAGGCTCAGTTATTTGCCAACTGTAAGATGACAACTGTAGA 1200
3235 ACACCATATGACTATCAAGGCTCAGTCTATCGTAACTGCAAGATGACAACTGTAGA 3294
1201 TGTGAGACCCCGGGGTATCATATCGCAAAATTTATGAGAACTGTGTCTCTAATAGAT 1260
3295 TGTGTAACCCCGGGGTATCATATCGCAAAATTTATGAGAACTGTGTCTCTAATAGAT 3354
1261 AGGCAATCATGCAATGCTCTATCTTACAGCAATTAATTTGAGGCTCAGTGGGGAATTT 1320
3355 AAACATCATGCAATGCTCTATCTTACAGCAATTAATTTGAGGCTCAGTGGGGAATTT 3414
1321 GATGCACTTTATCAAAAGAAATCTCAATACAGATTTCTAAGTAATCGTGACAGGCAAT 1380
3415 GATGCACTTTATCAAAAGAAATCTCAATACAGATTTCTAAGTAATTAATCAAGGCAAT 3474
1381 CTCGATATCTGACTGAGCTTGGGAATGTCACAACTCGATAGTAAGTAACTTGTAGATAAG 1440
3475 CTTGATATCTCACTGAGCTTGGGAATGTCACAACTCGATAGTAAGTAACTTGTAGATAAG 3534

1441 TTAGAGGAAGCAACAGCAAACTAGACAAAGTCAATGTCAAACTGACCAAGCACATCCGCT 1500
3535 TTAGAGGAAGCAACAGCAAACTAGACAAAGTCAATGTCAAACTGACCAAGCACATCTGCT 3594
1501 CTCATCACCTATATCGTTTAACTGTATATCTCTTGTGTTGTTGTTGTTGTTGTTGTTGTT 1560
3595 CTCATCACCTATATCGTTTAACTGTATATCTCTTGTGTTGTTGTTGTTGTTGTTGTTGTT 1620
1561 CTCATCACCTATATCGTTTAACTGTATATCTCTTGTGTTGTTGTTGTTGTTGTTGTTGTT 1620
3655 CTCATCACCTATATCGTTTAACTGTATATCTCTTGTGTTGTTGTTGTTGTTGTTGTTGTT 3714
1621 AATTAATACCTTGGATCAGATGAGAGCCACTACGAAATGTGA 1662
3715 AATTAATACCTTGGATCAGATGAGAGCCACTACGAAATGTGA 3756

RESULT 13

US-08-479-869-12
; Sequence 12, Application US/08479869
; Patent No. 6123949
; GENERAL INFORMATION:
; APPLICANT: Cochran Ph.D, Mark D
; TITLE OF INVENTION: Recombinant Fowlpox Virus S-FPV-043 and
; TITLE OF INVENTION: Uses Thereof
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: John P. White
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10112
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/479,869
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/024,156
; FILING DATE: 26-FEB-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: White Esq, John P
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212)977-9550
; TELEFAX: (212)664-0525
; TELEX: 422523
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4177 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHEetical: NO
; ANTI-SENSE: NO
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 115..1860
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 2095..3756
US-08-479-869-12

Query Match 85.0%; Score 1412.4; DB 3; Length 4177;
Best Local Similarity 90.6%; Pred. No. 0;
Matches 1506; Conservative 0; Mismatches 156; Indels 0; Gaps 0;

QY	1	ATGGGCTCAGATCTTCTTACACGAGTCCCGAGTACTCTGATGCTGACCGGTCCGGGTGCGG	60
Db	2095	ATGGGCTCCAGACCTTTCTACCAAGAACCCAGCACCTTAGTAGTGTGACTATACCGGGTTCGGG	2154
QY	61	CTGGCACTAGTTGGCGTCTGTCTCGCAAGCTCCCTTTGATGGCAGGCGCTTTTGACAGTGC	120
Db	2155	CTGGTACTGAGTTGCAATCTGTCTCGGCAACTCCATTTGATGGCAGGCGCTTTTGACAGTGC	2214
QY	121	GGGATTGTGTGTACAGGAGACAAAGCAGTCAACATATACACCTCATCTCAGACAGGGTCA	180
Db	2215	GGAATTGTGTGTACAGGAGACAAAGCAGTCAACATATACACCTCATCCACAGACAGATCA	2274
QY	181	ATCATAGTCAAGTTTACTCCCAATATATGCCCAAGATTAAGAGGGGTGTGCAAAAGCCCCG	240
Db	2275	ATCATAGTTAAGTCTCTCCGGAATCTGCCAAAGATTAAGAGGGCATGTGCGAAAGCCCCC	2334
QY	241	TTGGAGGCTACACAGGACATTGACTTTTCTCTACCCCTTCGTTGATTTCTATTCTT	300
Db	2335	TTGGATGATACAAACAGGACATTTGACCACTTTGCTACCCCTCTGGTGACTCTATCCGT	2394
QY	301	AGGATCAAGAGTCTGTGACTACATCTGGAGGAGGAAACAGGAGCGCTTTATAGCGCC	360
Db	2395	AGGATCAAGAGTCTGTGACTACATCTGGAGGAGGAGACAGGCGCTTTATAGCGCC	2454
QY	361	ATTATCGCGGTGAGCTCTCGGGTTTGAAACCGCTGCAAGATACAGCAGCTTCGGCT	420
Db	2455	ATTATTGGCGGTGTGGCTCTTTGGGGTTGCAACTGCCGCACAAATAACAGCGCGCGAGCT	2514
QY	421	CTGATACAGCCAAACAAATGCTGCCAATCCTCCGGCTTAAAGAGAGAAATTGCTGCA	480
Db	2515	CTGATACAGCCAAACAAATGCTGCCAATCCTCCGACTTAAAGAGAGCAATTGCGCA	2574
QY	481	ACCAATGAGGCTGTGCAAGAGTCACTGATGGATTATCAAACTAGCAGTGGCAGTTGGG	540
Db	2575	ACCAATGAGGCTGTGCATGAGTCACTGACGGATTATCGCAACTAGCAGTGGCAGTTGGG	2634
QY	541	AAGATGAGCAATTTGTTTAATGACGAGTTTAATAAAACAGCTCAGGAATTGGACTGTATA	600
Db	2635	AAGATGAGCAGTTTCGTTAATGACCAATTTAATAAAACAGCTCAGGAATTAGACTGCATC	2694
QY	601	AAATTTACCAGCAGGTTGGGTGTAGAACTCAACTGTATCTAATGATTTGACTACAGTA	660
Db	2695	AAATTTGCAAGCAAGTTGGTGTAGAGCTCAACTGTACTACCGGAATCGACTACAGTA	2754
QY	661	TTGGGGCCAAATCACTTCCCTTGCCTTAACCCAGCTGACTATCAGGCGCTTTACAAT	720
Db	2755	TTGGGACCAAAATCACTTCACTGCCTTAAACAAGCTGACTATTGAGGCACTTTACAAT	2814
QY	721	CTAGCTGGTGGGAATATGGAATTACTTTGTGACTAAGTTAGGTAGGGAACAACCACTC	780
Db	2815	CTAGCTGGTGGGAATATGGATTACTTTATTGACTAAGTTAGGTATAGGGAACAATCACTC	2874
QY	781	AGCTCATTAATTGGTAGCGGCTGATCACGGCAACCTTATCTGTACGACTCACAGACT	840
Db	2875	AGCTCATTAATCGGTAGCGGCTTAATCACCGGTAACCTTATTTATACGACTCACAGACT	2934
QY	841	CAGCTCTTGGGTATACAGGTAAACCTTACCCTCAGTCCGGGAACCTGGAATAATATGCGTGCC	900
Db	2935	CAACTCTTGGGTATACAGGTAACTTACTCTTCACTCGGGAACCTAATAATATATGCGTGCC	2994
QY	901	ACCTACTTGAACACCTTGTCTGTAAGTACAACAAAGGATTTGCCTCAGCACTCGTCCCA	960
Db	2995	ACCTACTTGAACACCTTATCCGTAAAGCACAAACAGGGGGAATTTGCCTCGGCACTTGTCCCA	3054
QY	961	AAGTGTGTATGAAGTTCGGTTCGTTGATAGAGAACTTGACACCTCATACTGTATAGAG	1020
Db	3055	AAAGTGTGTACAGGGTTCGGTTCGTTGATAGAGAACTTGACACCTCATACTGTATAGAA	3114
QY	1021	ACCGATTGGATCTATATTGTACAAGAAATAGTGAACATTCCTATGTCTCCTGGTATTAT	1080
Db	3115	ACTGACTTGAATTTATATTGTACAAGAAATAGTGAACATTCCTATGTCTCCTGGTATTAT	3174
QY	1081	TCCTGTTTGAGCGGCAATACATCGGCTTGTACTGTAAGACTGAAGCGGCACTCACT	1140

Db	3175	TCGTGCTTGAGCGGCAATACATCGGCGTGATGTACTCAAAGACCGAAGCGGCACCTTACT	3234
Qy	1141	ACGCGGTACATGACTCTCAAAGGCTCAGTTATTGGCCAACTGTAAGATGACAAACATGTAGA	1200
Db	3235	ACACCATATATGACTATCAAAGGCTCAGTCATCGCTAACTGCAAGATGACAAACATGTAGA	3294
Qy	1201	TGTGCAGACCCCCGGGTATCATATCGCAAAATATTGGAGAAGCTGTGCTCTTAATAGAT	1260
Db	3295	TGTGTAACCCCGCGGTATCATATCGCAAAACTATGGAGAAGCGTGCTCTTAATAGAT	3354
Qy	1261	AGGCAATCATGCAATGTCTCTATCCTTAGACGGAAATACTTTGAGGCTCAGTGGGGAATTT	1320
Db	3355	AAACAATCATGCAATGTTTTATCCTTAGGCGGGATAACTTTAAGGCTCAGTGGGGAATTC	3414
Qy	1321	GATGCAACTTATCAAAGGAATATCTCAATACAAGATTTCAAGTAATCGTGCAGGCAAT	1380
Db	3415	GATGTAACTTATCAGAAGAAATATCTCAATACAAGATTTCTCAAGTAATATAACAGGCAAT	3474
Qy	1381	CTCGATATCTCGACTGAGCTTTGGGAATGTCAAACAACCTCGATAAGTAATGCTTTAGATAAG	1440
Db	3475	CTTGATATCTCAACTGAGCTTTGGGAATGTCAAACAACCTCGATCAGTAACTTGAATAAG	3534
Qy	1441	TTAGAGAAAGCAACAGCAAACTAGACAAGGTCAATGTCAAACCTGACCAACATCCGCT	1500
Db	3535	TTAGAGAAAGCAACAGCAAACTAGACAAGGTCAATGTCAAACCTGACCAACATCTGCT	3594
Qy	1501	CTCATCACCTATATCGTTTAACTGTGCATATCTCTGTTTGTGCTATACCTAGGCTGGTT	1560
Db	3595	CTCATTAACCTATATCGTTTGTGCTATCATATCTCTGTTTGTGCTATACCTAGGCTGATT	3654
Qy	1561	CTAGCATGCTACCTGATGTACAAGCAAAAGCGCAACAGAGAAGCTTTGTTATGGCTTGGG	1620
Db	3655	CTAGCATGCTACCTTAATGTACAAGCAAAAGCGCAACAGAGAAGCTTTATGGCTTGGG	3714
Qy	1621	AATAATACCTGGATCAGATGAGAGCGCACCTACGAAATGTGA	1662
Db	3715	AATAATACCTAGATCAGATGAGAGCGCACCTACGAAATGTGA	3756

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RESULT 14
US-08-486-414-12
; Sequence 12, Application US/08486414B
; Patent No. 6136318
; GENERAL INFORMATION:
; APPLICANT: Cochran, Mark D.
; APPLICANT: Junker, David E.
; TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUSES AND USES THEREOF
; FILE REFERENCE: 42771D
; CURRENT APPLICATION NUMBER: US/08/486,414B
; CURRENT FILING DATE: 1995-06-07
; NUMBER OF SEQ ID NOS: 46
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 12
; LENGTH: 4177
; TYPE: DNA
; ORGANISM: Fowlpox virus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (115)..(1857)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (2095)..(3753)
US-08-486-414-12

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Query Match	85.0%	Score 1412.4	DB 3	Length 4177
Best Local Similarity	90.6%	Pred. No. 0		
Matches 1506	Conservative	0	Mismatches 156	Indels 0
Gaps	0			

Qy	1	ATGGGTCCTCCAGATCTTCTACAGGATCCCACTCTGATGCTGACCGTC	CGGGTGC	60
Db	2095	ATGGGTCCTCCAGATCTTCTACAGAACCCAGCACTATGATGCTGATC <td>TCGGGTC</td> <td>2154</td>	TCGGGTC	2154

QY 61 CTGGCACTGAGTGTGCTGTCGACAGCTCCCTTGATGGAGCGCTCTTGCACTGCA 120
DB 2155 CTGGTACTGAGTTGGATCTGTCGGCAAACTCCATTTGATGGAGCGCTCTTGCACTGCA 2214
QY 121 GGGATTGTTGGTACAGGAGACAAAGCAGTCAACATATATACACTCTCTCAGACAGGGTCA 180
DB 2215 GGAATTGTTGGTACAGGAGACAAAGCAGTCAACATATATACACTCTCTCAGACAGGATCA 2274
QY 181 ATCATAGTCAAGTTACTTCCAAATATGCGCAAGATGCGCAAGAGCGGTGTCGCAAGCCCGG 240
DB 2275 ATCATAGTCAAGTTACTTCCCGCAATCTGCGCAAGATGCGCAAGAGCGGTGTCGCAAGCCCGG 2334
QY 241 TTGGAGGGGTCAACAGGACATTTGACTTTTGTCTACCCCGCTTGGTATTCTATTCTGT 300
DB 2335 TTGATGATACAAAGGACATTTGACCTTTTGTCTACCCCGCTTGGTATTCTATTCTGT 2394
QY 301 AGGATACAAGAGTCTGTGACTACATCTGGAGAGGGAACAGGAGCGCTTTATAGGCGCC 360
DB 2395 AGGATACAAGAGTCTGTGACTACATCTGGAGAGGGAACAGGAGCGCTTTATAGGCGCC 2454
QY 361 ATTATCGGCGTGCAGCTCTCGGGTTCGACCGCTGCACAGATTAACAGAGCTTCGGCT 420
DB 2455 ATTATCGGCGTGTGCTTCTGCGGTTCGCACTCGCGCAAAATTAACAGCGCGCGCAGCT 2514
QY 421 CTGATACAAGCAACCAAAATGCTGCCAAATCTCTCCGGCTTAAAGAGAGAAATTGCTGCA 480
DB 2515 CTGATACAAGCAACCAAAATGCTGCCAAATCTCTCCGGCTTAAAGAGAGCAATTGCCGCA 2574
QY 481 ACCAATGAGGTGTGCAAGAGTCACTGATGATATCAAACTAGCAGTGGCGATTGGG 540
DB 2575 ACCAATGAGGTGTGCAAGAGTCACTGATGATATCAAACTAGCAGTGGCGATTGGG 2634
QY 541 AAGATGAGCAATTTGTTAATGACCAAGTTTAAATAAACAGCTCAGGAATTGCACTGATA 600
DB 2635 AAGATGAGCAATTTGTTAATGACCAAGTTTAAATAAACAGCTCAGGAATTGCACTGATA 2694
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DB 2695 AAAATTACCCAGAGTGTGGTGTAGAACTCAACCTGTATCTAAGTGAATGACTACAGTA 2754
QY 661 TTCGGGCCAATAACACTTCCCTTCCCTTAAACAGCTGACTATCCAGGCGCTTTACAAAT 720
DB 2755 TTCGGGCCAATAACACTTCCCTTCCCTTAAACAGCTGACTATTTACGACACTTTTACAAAT 2814
QY 721 CTAGCTGTGGGAATATGATGATTTACTTGTGTAAGTGTAGTGGGAACCAACCACTC 780
DB 2815 CTAGCTGTGGGAATATGATGATTTACTTGTGTAAGTGTAGTGGGAACCAACCACTC 2874
QY 781 AGCTCAITTAATTTGAGCGGCTGATACACCGGCAACCTTATCTGTAGCTCAGACT 840
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QY 841 CAGCTTTGGTATACAGTAAACCTTACCCTCAGTGGGAACCTGAAATTAATGCGTGC 900
DB 2935 CAACCTTTGGTATACAGTAACTTACCCTCAGTGGGAACCTTAAATTAATGCGTGC 2994
QY 901 ACCTACTTGGAAACCTTGTGTAAGTACCAACAGGATTTGCTCAGCACTGCTCCCA 960
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DB 3115 ACTGACTTAGATTTATATTGTACAGATAGTGAATTCCTATGTCTCTGTTGTTAT 3174
QY 1081 TCCTGTTTGGCGGCAATACATCGCTTGTGATGTAAGTGTGTAAGTGTGTAAGTGTGTAAG 1140
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DB 3235 ACACATATATGACTATCAAGGCTCAGTATCGTAACTGCAAGATGACAACTGTAGA 3294
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QY 1321 GATGCAATCTTCAAAAGATATCTCAATACAAATCTCAAGTAATCGTGACAGGCAAT 1380
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QY 1501 CTCATCACTATATCGTTTAACTGTCTATATCTCTGTTTCTGTTTATAGCTGCTGTT 1560
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QY 1561 CTAGATGCTACCTGATGTCAAGAAAGGCGCAACAGAGACTTGTGTTAGCTTGGG 1620
DB 3655 CTAGATGCTACCTGATGTCAAGAAAGGCGCAACAGAGACTTGTGTTAGCTTGGG 3714
QY 1621 AATATACCTGATGATGATGAGAGGCGCACTGACCAAGTAATGTGA 1662
DB 3715 AATATACCTGATGATGATGAGAGGCGCACTGACCAAGTAATGTGA 3756

RESULT 15

PCT-US94-01826A-12
; Sequence 12, Application PC/TUS9401826A
; GENERAL INFORMATION:
; APPLICANT: Syntro Corporation, et al.
; TITLE OF INVENTION: Recombinant Fowlpox Virus S-PPV-043 and Uses Thereof
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: John P. White
; STREET: 30 Rockefeller Plaza
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10112
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/01826A
; FILING DATE: 28-FEB-1994
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: White Esq, John P
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212)977-9550
; TELEFAX: (212)664-0525
; TELEX: 422523
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4177 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO

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; ANTI-SENSE: NO
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 115..1860
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 2095..3756
PCT-US94-01826A-12

Query Match      85.0%; Score 1412.4; DB 5; Length 4177;
Best Local Similarity 90.6%; Pred. No. 0;
Matches 1506; Conservative 0; Mismatches 156; Indels 0; Gaps 0;

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Job time : 153 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: April 17, 2004, 06:54:07 ; Search time 691 Seconds
(without alignments)
10762.306 Million cell updates/sec

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Perfect score: 1662
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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2890132 seqs, 2237290429 residues

Total number of hits satisfying chosen parameters: 5780264

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications NA:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	1452.4	87.4	1662	14	US-10-229-412-10
3	1431.6	86.1	15882	12	US-10-440-419-56
4	1417.2	85.3	15900	12	US-10-440-419-55
5	1412.4	85.0	15186	10	US-09-741-744A-134
6	1412.4	85.0	15186	14	US-10-377-718-3
7	1412.4	85.0	15186	15	US-10-429-735-3
8	1375.4	82.8	3570	9	US-09-881-457A-1
9	162.2	9.8	15492	9	US-09-733-692A-60
10	162.2	9.8	15498	9	US-09-733-692A-62
11	162.2	9.8	15498	9	US-09-733-692A-61
12	92.8	5.6	1986	12	US-10-670-695-35
13	92.8	5.6	2113	10	US-09-951-061A-86
14	92.8	5.6	4343	10	US-09-951-061A-91
15	92.8	5.6	4604	10	US-09-951-061A-93

16	87.8	5.3	692	14	US-10-206-901B-50	Sequence 50, Appl
17	84.2	5.1	2384	15	US-10-397-635-8	Sequence 8, Appl
18	82.6	5.0	1653	9	US-09-873-233A-17	Sequence 17, Appl
19	81	4.9	1653	9	US-09-873-233A-19	Sequence 19, Appl
20	56.2	3.4	15456	10	US-09-900-112-35	Sequence 35, Appl
21	56.2	3.4	15456	10	US-09-900-112-36	Sequence 36, Appl
22	40.4	2.4	1620	15	US-10-371-264-25	Sequence 25, Appl
23	40.4	2.4	1620	15	US-10-371-099-321	Sequence 321, Appl
24	40.4	2.4	1620	15	US-10-371-122-321	Sequence 321, Appl
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26	40.4	2.4	13135	15	US-10-371-264-97	Sequence 97, Appl
27	40.4	2.4	13135	15	US-10-371-099-21	Sequence 21, Appl
28	40.4	2.4	13135	15	US-10-371-122-21	Sequence 21, Appl
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30	39.2	2.4	1620	15	US-10-371-264-23	Sequence 23, Appl
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32	39.2	2.4	1620	15	US-10-371-122-319	Sequence 319, Appl
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34	39.2	2.4	13215	15	US-10-371-264-96	Sequence 96, Appl
35	39.2	2.4	13215	15	US-10-371-099-20	Sequence 20, Appl
36	39.2	2.4	13215	15	US-10-371-122-20	Sequence 20, Appl
37	39.2	2.4	13215	15	US-10-373-567-96	Sequence 96, Appl
38	38.2	2.3	8726	9	US-09-070-927A-95	Sequence 95, Appl
39	38	2.3	811	14	US-10-184-644-414	Sequence 414, Appl
40	38	2.3	811	14	US-10-184-634-414	Sequence 414, Appl
41	38	2.3	950	12	US-10-027-632-258267	Sequence 258267,
42	38	2.3	950	12	US-10-027-632-258268	Sequence 258268,
43	38	2.3	950	12	US-10-027-632-258269	Sequence 258269,
44	38	2.3	950	12	US-10-027-632-258270	Sequence 258270,
45	38	2.3	950	12	US-10-027-632-258271	Sequence 258271,

ALIGNMENTS

RESULT 1
US-09-784-990-10
; Sequence 10, Application US/09784990
; Patent No. US20020037292A1
; GENERAL INFORMATION:
; APPLICANT: AUDONNET, JEAN-CHRISTOPHE
; APPLICANT: BOUCHARON, ANNABELLE
; APPLICANT: RIVIERE, MICHEL
; TITLE OF INVENTION: AVIAN POLYNUCLEOTIDE VACCINE FORMULA
; FILE REFERENCE: 454313-2260
; CURRENT APPLICATION NUMBER: US/09/784,990
; CURRENT FILING DATE: 2001-02-16
; PRIOR APPLICATION NUMBER: 96/09339
; PRIOR FILING DATE: 1996-07-19
; PRIOR APPLICATION NUMBER: PCT/FR97/01326
; PRIOR FILING DATE: 1997-07-16
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 10
; LENGTH: 1662
; TYPE: DNA
; ORGANISM: Newcastle disease virus
US-09-784-990-10

Query Match	87.4%	Score 1452.4;	DB 9;	Length 1662;
Best Local Similarity	92.1%	Pred. No. 0;		
Matches 151;	Conservative	0;	Mismatches 131;	Indels 0;
Gaps	0;			
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US-01-229-412-10
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; Publication No. US2003012415A1
; GENERAL INFORMATION:
; APPLICANT: AUDONNET, JEAN-CHRISTOPHE
; APPLICANT: BOUCHARDON, ANNABELLE
; APPLICANT: RIVIERE, MICHEL
; TITLE OF INVENTION: AVIAN POLYNUCLEOTIDE
; FILE REFERENCE: 454313-2260
; CURRENT APPLICATION NUMBER: US/10/229,412
; CURRENT FILING DATE: 2002-08-28
; PRIOR APPLICATION NUMBER: US/09/232,479
; PRIOR FILING DATE: 1999-01-15
; PRIOR APPLICATION NUMBER: 96/09339
; PRIOR FILING DATE: 1996-07-19
; PRIOR APPLICATION NUMBER: PCT/FR97/01326
; PRIOR FILING DATE: 1997-07-16
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 10
; LENGTH: 1662
; TYPE: DNA
; ORGANISM: Newcastle disease virus
US-01-229-412-10

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	Query Match	87.4%	Score 1452.4;	DB 14;	Length 1662;
	Best Local Similarity	92.1%;	Pred.No. 0;	Mismatches 1531;	Conservative 0;
				Gaps 0;	
Qy	1	ATGGGCTCCAGTCTTTACACGATCCCAGTACTCTGTATGCTGACCGTCGGGTGC	60		
Dd	1	ATGGGCTCCAGTCTTTACACGATCCCAGTACTCTAAATGCTGATCCTCCGAACCGC	60		
Qy	61	CTGGCACTGAGTTGCGTCTTGCGACAAGCTCCCTTGATGGCAGGCCCTTTGCACTGCA	120		
Dd	61	CTGACACTGAGCTGTATCCGCTTGACAAGCTCTCTTGATGGCAGGCCCTTTGCGGCTCA	120		
Qy	121	GGGATTGCTGGTGACAGAGACAAGAAGTCAAATATACACCTCATCTCAGACAGGGTCA	180		
Dd	121	GGGATCTGGTTAACAGGAGATAAAGCAGTCAACATATACACCTCATCTCCAGACAGGGTCA	180		
Ov	181	ATCATAGTCAAGTTTACTTCCCAATATATGCCAAAGATAAAGAGGGGTGTGAAAAAGCCCCG	240		

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Db 181 ATCATAGTTAAGTTACTCCGGAATATGCCAGAGCAAGAGGTTGTGCAAAAGCCCCA 240
Qy 241 TTGAGGCGTACAAAGAGCAATGACTACTTTGCTCACCCCTTGTGTGATTTCTATTGCT 300
Db 241 TTGAGGCGTACAAAGAGCAACTGACTACTTTTACTCACCCCTTGTGTGATTTCTATCCG 300
Qy 301 AGGATACAAGAGTCTGTGACTACATCTGGAGGAGGAAACAGGACGCTTATAGGCGCC 360
Db 301 AGGATACAAGAGTCTGTGACTACTTTCCGGAGGAGGAGACAGACGCTTATAGGTCGC 360
Qy 361 ATTATCGGCGTGCAGCTCTCGGGTTGCAACCGCTGCACAGATAACAGCAGCTTCGGCT 420
Db 361 ATTATCGGCGTGTAGCTCTCGGGTTGCGACAGCTGCACAGATAACAGCAGCTTCGGCC 420
Qy 421 CTGATAAGCAACCAAAATGTCGCAACATCTCCGGCTTAAAGAGAGAAATGCTGCA 480
Db 421 CTGATAAGCAACCAAGATGCTGCCAACATCTCCGGCTTAAAGAGAGCAATGCTGCA 480
Qy 481 ACCAATGAGCTGTGCAGAGTCACTGATGGATTATCAAACTAGCAGTGGCAGTTGGG 540
Db 481 ACCAATGAGCTGTGCAGAGTCACTGATGGATTATCAAACTAGCAGTGGCAGTTAGG 540
Qy 541 AAGATGCAAGCAATTTGTTAATGACAGCTTTAATAAAGCAGCTCAGGAATGGACTGTATA 600
Db 541 AAGATGCAAGCAATTTGTTCAATGACCACTTCAATAATACAGCGCAAGATGGACTGTATA 600
Qy 601 AAAATTACCAGCAGGTTGGTGTAGAACTCAACTGTATCTAATGAAATGACTACAGTA 660
Db 601 AAAATTGACAGCAGGTCGGTGTAGAACTCAACTGTGTACCTAATGAAATGACTACAGTA 660
Qy 661 TTGGGGCCAAATCACTCCCGTCCCTTAACCCAGCTGACTATCCAGGCGCTTTACAAT 720
Db 661 TTGGGGCCAAATCACTCCCGTCCCTTAACCCAGCTGACTATCCAGGCGCTTTACAAT 720
Qy 721 CTAGCTGGTGGGAATATGGAATTAATCTGACTAAGTTAGTGTAGGGAACAACCAACTC 780
Db 721 CTAGCTGGTGGTAATATGGAATTAATCTGACTAAGTTAGTGTAGGGAACAACCAACTC 780
Qy 781 AGCTCATTAATTTGTTAGCGGCTGATCACGGCAACCCCTATTTCTGTACGACTCACAGACT 840
Db 781 AGCTCATTAATTTGTTAGCGGCTTGTATCAAGCAACAACCAAGGATTTGCTTACGACTCACAGACT 840
Qy 841 CAGCTCTTGGGTATACAGGTAAACCTACCTCAGTCGGGAACCTGAATATATGCGTGCC 900
Db 841 CAGATCTTGGGTATACAGGTAACTTTGCCCTCAGTTGGGAACCTGAATATATGCGTGCC 900
Qy 901 ACCTACTTGAACCTTTGCTGTAAGTACAAACCAAGGATTTGCTCAGCACTCGTCCCA 960
Db 901 ACCTACCTGGAGACTTATCTGTAAGCAACAACCAAGGATTTGCCCTCAGCACTGTGCCA 960
Qy 961 AAGGTGTGATGAGTTCGGTTCGGTGTATAGAGAACTTGACACCTCATCTGATAGAG 1020
Db 961 AAGGTGTGATGACAGGTTCGGTTCGGTGTATAGAGAACTTGACACCTCATCTGATAGG 1020
Qy 1021 ACCGATTTGATCTATATGTAAGAAATAGTGCATTCCTATGCTCTCGTGTATTAT 1080
Db 1021 ACCGATTTGATTTATCTGTAAGAAATAGTGCATTCCTATGCTCTCGTGTATTAT 1080
Qy 1081 TCCTGTTTGAAGCGCAATACATCGGCTTGCATGTACTCGAAGACTGAAGCGCACTCACT 1140
Db 1081 TCCTGTTGAGCGGTAATACATCGGCTTGCATGTACTTCGAAGACTGAAGCGCACTTACT 1140
Qy 1141 ACGCCGTACATGACTCTCAAGGCTCAGTTATGCGCAACTGTGATGACAAATGATGAA 1200
Db 1141 ACGCCATATATGGCTCTCAAGGCTCAGTTATGCGCAATTTGCAAGCTGACAAATGATGAA 1200
Qy 1201 TGTGCAGACCCCGGCTATCATATCGAAATTTATGGAGAGCTGTCTCTTAATAGAT 1260
Db 1201 TGTGCAGATCCCCAGGATATCATATCGAAATTTATGGAGAGCTGTCTCTTAATAGAT 1260
Qy 1261 AGGCAATCATGCAATGCTTATCTCTTACGCGGAATTAATTTAGGCTCAGTGGGAATTT 1320
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Db 1261 AGGCACTCATGCAACGCTTCTATCTCTAGACGGGATAAATCTTGAGGCTCAGTGGGAATTT 1320
Qy 1321 GATGCAACTTTATCAAAAGAATATCTCAATCAAGATTCTCAAGTAATCTGTGACAGGCAAT 1380
Db 1321 GATGCAACTTATCAAAAGAATATCTCTATACTAGATTCTCAAGTTATAGTGACAGGCAAT 1380
Qy 1381 CTGATATCTCGACTGAGCTTGGGAATGTCAACNACTCGATAGTAATGCTTTAGATAAG 1440
Db 1381 CTTGATATATCAACTGAGCTTGGGAATGTCAACNACTCAATAAGTAATGCTTGAATAAG 1440
Qy 1441 TTAGAGAAAGCAACAGCAAACTAGACAAGGTCAATGCTCAAACTGACCAAGCACATCGCT 1500
Db 1441 TTAGAGAAAGCAACAGCAAACTAGACAAGGTCAATGCTCAAACTGACCAAGCACATCTGCT 1500
Qy 1501 CTCAATCACTATATCGTTTAACTGTGCATATCTCTCTTTTGTGTGATACTTAGCTTGTT 1560
Db 1501 CTCAATCACTATACGTTTAACTGTGCATATCTCTCTTTTGTGTGATACTTAGCTTGTT 1560
Qy 1561 CTAGCATGCTACCTGATGTACAGCAAAAGCGCAACAGAGACCTTGTATGCTTGGG 1620
Db 1561 CTAGCATGCTACCTGATGTACAGCAAAAGCGCAACAGAGACCTTGTATGCTTGGG 1620
Qy 1621 AATAAATACCTGGATCAGATGAGAGCCACTACGAAAATGTGA 1662
Db 1621 AATAAATACCTTGTATGATGAGAGCCACTACGAAAATGTGA 1662
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RESULT 3

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US-10-440-419-56
; Sequence 56, Application US/10440419
; Publication No. US20030224017A1
; GENERAL INFORMATION:
; APPLICANT: SAMAL, SIBA K.
; APPLICANT: HUANG, ZHUHUI
; TITLE OF INVENTION: RECOMBINANT NEWCASTLE DISEASE VIRUSES USEFUL AS
; FILE REFERENCE: 108172-00096
; CURRENT APPLICATION NUMBER: US/10/440,419
; CURRENT FILING DATE: 2003-05-19
; PRIOR APPLICATION NUMBER: 09/926,431
; PRIOR FILING DATE: 2002-03-06
; PRIOR APPLICATION NUMBER: PCT/US00/06700
; PRIOR FILING DATE: 2000-05-05
; PRIOR APPLICATION NUMBER: 60/381,462
; PRIOR FILING DATE: 2002-05-17
; PRIOR APPLICATION NUMBER: 60/171,072
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: 60/132,597
; PRIOR FILING DATE: 1999-05-05
; NUMBER OF SEQ ID NOS: 56
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 56
; LENGTH: 15882
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Recombinant cDNA for NDV
US-10-440-419-56
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Query Match 86.1%; Score 1431.6; DB 12; Length 15882;
Best Local Similarity 91.3%; Pred.No. 0;
Matches 1518; Conservative 0; Mismatches 144; Indels 0; Gaps 0;

Qy 1 ATGGGCTCCAGATCTTCTTACCAGATCCCAAGTACCTCTGATGTGACCGTCCGGGTCGCG 60
Db 4544 ATGGGCCCCAGACCTTCTACCAAGAACCCAGTACCTATGATGCTGACTGCTCCAGTCCG 4603
Qy 61 CTGGCACTGAGTTGCTGTCGCAAGCTCCCTTGTAGTGAGGAGGCTCTTGCAGTGC 120
Db 4604 CTGGTACTGAGTTGCTGTCGCGCAAACTCCATTTGATGGCAGGCTCTTGGCGGTGCA 4663
Qy 121 GGGATTTGGTGTACAGGAGCAAGCAGTCAACATATACCTCATCTCAGACAGGTC 180
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4664 GGAATTGGTAAACAGGAGACAAAGCAGTCAACATATATACACTCCAGACAGGATCA 4723
181 ATCATAGTCAAGTTACTCCAAATATGCCCCAAAGATAAAGAGGCGTGTGCAAAAGCCCG 240
4724 ATCATAGTTAAGTCTCTCCAAACCTGCCAAAGGATAAGGAGGCATGTGCGAAAGCCCCC 4783
241 TTGGAGGCGTCAACAGGACATTTGACTACTTTTGGCTCACCCCTTGGTGTATTCTATTGGT 300
4784 TTGGATGATACAAACAGACATTTGACCACTTTTGGCTCACCCCTTGGTGTATTCTATTGGT 4843
301 AGGATCAAGAGTCTGTGACATACATCTGGAGAGGAAACAGGAGCGCTTATAGGCGCC 360
4844 AGGATCAAGAGTCTGTGACATACATCTGGAGAGGAAACAGGAGCGCTTATAGGCGCC 4903
361 ATTATCGGCGGTGAGCTCTCGGCGTTGCAACCGCTGCACAGATTAACAGCAGCTTCGGCT 420
4904 ATTATCGGCGGTGAGCTCTCGGCGTTGCAACCGCTGCACAGATTAACAGCAGCTTCGGCT 4963
421 CTGATACAAAGCAACCAAAATGCTGCCAACATCTCCCGCTTAAAGAGAGAAATTCCTGCA 480
4964 CTGATACAAAGCAACCAAAATGCTGCCAACATCTCCCGCTTAAAGAGAGCAATTCGCCGA 5023
481 ACCAATGAGGTGTGCAAGAGTCACTGATGAGTATCAAACTAGAGTGGCAGTTGGG 540
5024 ACCAATGAGGCGTGCATGAGTCACTGACGAGTATCGCAACTAGCAGTGGCAGTTGGG 5083
541 AAGATGACGCAATTTGTTAATGACCACTTAAATGAAGAGTCAAGCTCAGGAATTCGACTGATA 600
5084 AAGATGACGCAATTTGTTAATGACCACTTAAATGAAGAGTCAAGCTCAGGAATTCGACTGATA 5143
601 AAAATTACCCAGCAGTGGTGTAGAACTCAACCTGTGTATCAACTGGAATTCAGTACAGTA 660
5144 AGAATTGCACAGCAAGTGGTGTAGAGTCAACCTGTACCTTAACCGAATTCAGTACAGTA 5203
661 TTGGGCGCAAAATCACTTCCCTGCTTAAACCAAGTCACTATTCAGGCACTTTACAAT 720
5204 TTGGGCGCAAAATCACTTCCCTGCTTAAACCAAGTCACTATTCAGGCACTTTACAAT 5263
721 CTAGCTGTGGGAATATGATTTACTTGTGATGAGTGTAGTGTAGGGAACCAACCACTC 780
5264 CTAGCTGTGGGAATATGATTTACTTGTGATGAGTGTAGTGTAGGGAACCAACCACTC 5323
781 AGCTCAATTAATTTGGTGTAGGCGCTGTATCAACCGCAACCTTATCTGTACGACTCAGACT 840
5324 AGCTCAATTAATTTGGTGTAGGCGCTGTATCAACCGCAACCTTATCTGTACGACTCAGACT 5383
841 CAGCTCTTGGGTATACAGTAACTTACCTCAGTCGGGAACCTGAATTAATGCGTGGC 900
5384 CAACCTCTTGGGTATACAGTAACTTACCTCAGTCGGGAACCTGAATTAATGCGTGGC 5443
901 ACCTACTTGGAAACCTTCTGTGTAAGTACACCAAGGATTTGCTCAGCAGCTGTCGCA 960
5444 ACCTACTTGGAAACCTTCTGTGTAAGTACACCAAGGATTTGCTCAGCAGCTGTCGCA 5503
961 AAGTGTGTGATGAAGGTCGGTTCGGTGTAGAGAACTTGACACCTCATCTGTATAGAG 1020
5504 AAGTGTGTGATGAAGGTCGGTTCGGTGTAGAGAACTTGACACCTCATCTGTATAGAG 5563
1021 ACCGATTTGGATCTATATGTAAGATAGTGAATTCCTCCTATGTCCTGGTATTAT 1080
5564 ACCGATTTGGATCTATATGTAAGATAGTGAATTCCTCCTATGTCCTGGTATTAT 5623
1081 TCCTGTTTGGAGCGCAATACATCGGCTGTGATGTAAGTGTGCAAGCTGAAGCGCACTCACT 1140
5624 TCCTGTTTGGAGCGCAATACATCGGCTGTGATGTAAGTGTGCAAGCTGAAGCGCACTCACT 5683
1141 ACGCGGTATACATCTCTCAAGGCTCAGTATTATGCGCAACTGTAAGATGCAACATGTAGA 1200
5684 ACGCGGTATACATCTCTCAAGGCTCAGTATTATGCGCAACTGTAAGATGCAACATGTAGA 5743
1201 TGTGCAAGCCCCCGGTATCATATCGCAAAATTTATGAGAGCTGTCTCTATATAGAT 1260
5744 TGTGTAACCCCCCGGTATCATATCGCAAAATTTATGAGAGCTGTCTCTATATAGAT 5803

1261 AGGCAATCATGCAATGCTCTATCCTTAGACGGAATAACTTTTCAAGCTCAGTGGGAATTT 1320
5804 AAGCAATCATGCAATGCTCTATCCTTAGACGGAATACTTTTAAAGCTCAGTGGGAATTC 5863
1321 GATGCAACTTATCAAAAGATATCTCAATACAAAGATTTCTCAAGTAAATCGTGACAGGCAAT 1380
5864 GATGCAACTTATCAAAAGATATCTCAATACAAAGATTTCTCAAGTAAATTAACAGGCAAT 5923
1381 CTCGATATCTGACATGAGCTTGGGAATGTCAAACTCGATAAGTAATGCTTTAGATAG 1440
5924 CTTGATATCTCAACTGAGCTTGGGAATGTCAAACTCGATCAAGTAAATGCTTTGAATAG 5983
1441 TTAGAGGAAGCAACAGCAAACTAGACAAAGTCAATGTCAAACTGACAGCAATCCGCT 1500
5984 TTAGAGGAAGCAACAGCAAACTAGACAAAGTCAATGTCAAACTGACAGCAATCTGCT 6043
1501 CTCATCACTATATGCTTTTAACTGTCTATCTCTTGTGTGTATCTTAGCTGCTT 1560
6044 CTCATCACTATATGCTTTTAACTGTCTATCTCTTGTGTGTATCTTAGCTGCTT 6103
1561 CTAGATGCTACCTGATGTACAAAGCAAGGCGCAAGAGACCTTGTATGCTTGGG 1620
6104 CTAGATGCTACCTGATGTATAGCAAAAGGCGCAAGAGACCTTGTATGCTTGGG 6163
1621 AATAATACCTGGATCAGATCAGAGGCACTACGAAATGTGA 1662
6164 AATAATACCTGGATCAGATCAGAGGCACTACGAAATGTGA 6205

RESULT 4

US-10-440-419-55
; Sequence 55, Application US/10440419
; Publication No. US20030224017A1
; GENERAL INFORMATION:
; APPLICANT: SAMAL, SIBA K.
; APPLICANT: HUANG, ZHUHUI
; TITLE OF INVENTION: RECOMBINANT NEWCASTLE DISEASE VIRUSES USEFUL AS
; FILE REFERENCE: 108172-00096
; CURRENT APPLICATION NUMBER: US/10/440,419
; CURRENT FILING DATE: 2003-05-19
; PRIOR APPLICATION NUMBER: 09/926,431
; PRIOR FILING DATE: 2002-03-06
; PRIOR APPLICATION NUMBER: PCT/US00/06700
; PRIOR FILING DATE: 2000-05-05
; PRIOR APPLICATION NUMBER: 60/381,462
; PRIOR FILING DATE: 2002-05-17
; PRIOR APPLICATION NUMBER: 60/171,072
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: 60/132,597
; PRIOR FILING DATE: 1999-05-05
; NUMBER OF SEQ ID NOS: 56
; SOFTWARE: Patent in Ver. 2.1
; SEQ ID NO 55
; LENGTH: 15900
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Recombinant cDNA for NDV
US-10-440-419-55

Query Match 85.3%; Score 1417.2; DB 12; Length 15900;
Best Local Similarity 90.8%; Pred. No. 0;
Matches 1509; Conservative 0; Mismatches 153; Indels 0; Gaps 0;
QY 1 ATGGGCTCCAGATCTTACAGGATCCAGTACCTCTGATGCTGACCGCTCGGGTTCGG 60
DB 5258 ATGGGCTCCAGATCTTACCAAGAACCCAGCACCTATGATGCTGACTATCGGGTTCGG 5317
QY 61 CTGGCAGCTGAGTGGCTGTGCGCAAGCTCCCTTGTATGCGAGGCTCTTTCAGCTGCA 120
DB 5318 CTGGTACTGAGTTGATCTGTCCGGCAAACTCCATGTATGCGAGGCTCTTTCAGCTGCA 5377

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QY 121 GGGATTGGTGACAGGAGACAAAGCAGTCAACATATACACTCATCTCAGACAGGGTCA 180
Db 5378 GGAATTGGTTACAGGAGACAAAGCCGCTCAACATATACACTCATCTCAGACAGGGTCA 5437
QY 181 ATCATAGTCAAGTTACTCCCAAAATATGCCAAAGATAAAGAGGGGTGTGCAAAAGCCCGC 240
Db 5438 ATCATAGTCAAGTTCCTCCGAACTGCCCCAAGATAGAGGAGCATGTGCGAAGCCCCC 5497
QY 241 TTGAGGCGGTACACAGGACATTGACTACTTTGTCTACCCCCCTTGGTGATCTTATTCGT 300
Db 5498 TTGATGCGATACAAAGGACATTGACCACTTTGTCTACCCCCCTTGGTGATCTTATTCGT 5557
QY 301 AGGATACAAGAGTCTGTGACTACATCTGGAGGAGGAAACAGGACGCCCTTATAGGCGCC 360
Db 5558 AGGATACAAGAGTCTGTGACTACATCTGGAGGAGGAGAGAGGGCGCCCTTATAGGCGCC 5617
QY 361 ATTATCGGCGGTGAGCTCTCGGGGTTGCAACCGCTGCACAGATAAACAGCAGCTTCGGCT 420
Db 5618 ATTATCGGCGGTGAGCTCTCGGGGTTGCAACTGCCGACAAATAACAGCGCGCCGAGCT 5677
QY 421 CTGATACAAGCCACCAAAATGCTGCCAAGATCTCTCGGCTTAAAGAGAGAAATTCGTGCA 480
Db 5678 CTGATACAAGCCACCAAAATGCTGCCAAGATCTCTCGGCTTAAAGAGAGCAATTCGCGCA 5737
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Db 5738 ACCAATGAGGCTGTGATGAGTCACTGACGGATTATCGCAACTAGCAGTGGCAGTTGGG 5797
QY 541 AAGATGAGCAAAATTTGTTAATGACAGTTTAAATGACAGCTCAGGAATTTGGAATGATA 600
Db 5798 AAGATGAGCAAGTTTGTATGACCAATTTAATGACCACTTAAATGACAGCTCAGGAATTTAGATGCAATC 5857
QY 601 ABAATTACCAGCAGGTTGGTGTAGAACTCAACTGTATCTAAGTGAATTCAGTACAGTA 660
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Db 5918 TTGGGACCAAAATCACTTCACTGCTTTAAAGAGTGAATTCAGGCACTTTACAAT 5977
QY 721 CTAGCTGGTGGGAATATGGAATTAATGCTGACTAAGTTAGTGTAGGAGAAACCAACTC 780
Db 5978 CTAGCTGGTGGGAATATGGAATTAATGCTGACTAAGTTAGTGTAGGAGAAACCAACTC 6037
QY 781 AGCTCATTAATGCTAGCGGCTGATCACCGGCAACCTTATCTGTAGACTCAAGACT 840
Db 6038 AGCTCATTAATGCTAGCGGCTTAAATCACCGGTAAACCTTATCTGTAGACTCAAGACT 6097
QY 841 CAGCTCTTGGGTATACAGGTAAACCTTACCTCAGTCCGGAACTGAATAATATGCGNGCC 900
Db 6098 CAACTCTTGGGTATACAGGTAACTTACCTCAGTCCGGAACTGAATAATATGCGNGCC 6157
QY 901 ACCTACTTGGAAACCTTATCGGTAAAGCAACCAAGGAGTTTGCCTCGGCACCTTGTCCCA 960
Db 6158 ACCTACTTGGAAACCTTATCGGTAAAGCAACCAAGGAGTTTGCCTCGGCACCTTGTCCCA 6217
QY 961 AAGTGTGTATGAGTGGTTCGTTGATAGAGAACTTGACACCTCATCTGATATAGAG 1020
Db 6218 AAGTGTGTATGAGTGGTTCGTTGATAGAGAACTTGACACCTCATCTGATATAGAG 6277
QY 1021 ACCGATTGGATCTATATTGTACAAGAAATAGTGACATTCCTATGTCTCTCTGGTATTAT 1080
Db 6278 ACTGACTTGAATTTATTTGTAAGAATATAGTAACTTCCCTATGTCTCTCTGGTATTAT 6337
QY 1081 TCCGTTTGGACGCAATATACGCTTGGATGATGCTGAAAGTGAAGGCGCACTCACT 1140
Db 6338 TCCGTTTGGACGCAATATACGCTTGGATGATGCTGAAAGTGAAGGCGCACTCACT 6397
QY 1141 ACGCCGTGATGACTCTCAAGGCTCAGTTATTGCGCAACTGTATGATGACAAATGATGAG 1200
Db 6398 ACACCATACATGACTCAAGGTTTCACTCATGCCAACTGCAAGATGACAAATGATGAG 6457
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QY 1201 TGTGCAACCCCGGGGTATCATATCGCAAAATATTGAGAGAGCTGTGTCTCTTAATAGAT 1260
Db 6458 TGTGTAACCCCGGGGTATCATATCGCAAAATATTGAGAGAGCTGTGTCTCTTAATAGAT 6517
QY 1261 AGGCAATCATCAATGCTCTATCTTACAGCGGAATAACTTTGAGGCTCAGTGGGAAATTT 1320
Db 6518 AAGCAATCATCAATGCTCTATCTTACAGCGGAATAACTTTGAGGCTCAGTGGGAAATTT 6577
QY 1321 GATCAACTTATCAAAAGAAATATCTCAATACAAGATTTCTCAAGTAATCTGACAGGCAAT 1380
Db 6578 GATCAACTTATCAAAAGAAATATCTCAATACAAGATTTCTCAAGTAATTAATAACAGGCAAT 6637
QY 1381 CTCGATATCTCGACTGAGCTTGGGAATGTCAAACTCGATAAGTAATGCTTTAGATAAG 1440
Db 6638 CTTGATATCTCAACTGAGCTTGGGAATGTCAAACTCGATCAGTAATGCTTTAGATAAG 6697
QY 1441 TTAGAGAAAGCAACAGCAAACTAGACAGGTCAATGTCAAACTGACCAAGCACATCCGCT 1500
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QY 1501 CTATCACTTATATCGTTTAACTGTATATCTCTTGTGTGTATATCTTAGCTCGTT 1560
Db 6758 CTATCACTTATATCGTTTAACTGTATATCTCTTGTGTGTATATCTTAGCTCGTT 6817
QY 1561 CTAGCATGCTACCTGATGTACAGCAAGCGCAACAGAGACCTTGTATGCTTTGGG 1620
Db 6818 CTAGCATGCTACCTGATGTACAGCAAGCGCAACAGAGACCTTGTATGCTTTGGG 6877
QY 1621 AATAATACCTTGGATCAGATGAGAGCCACTACGAAATGTGA 1662
Db 6878 AATAATACCTTGGATCAGATGAGAGCCACTACGAAATGTGA 6919
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RESULT 5
US-09-741-744A-134
; Sequence 134, Application US/09741744A
; Publication No. US20030087417A1
; GENERAL INFORMATION:
; APPLICANT: Peeters, Bernadus
; APPLICANT: de Leeuw, Olav
; APPLICANT: Klaus, Guus
; APPLICANT: Arnoud, Gielkens
; TITLE OF INVENTION: Newcastle Disease Virus Infectious Clones, Vaccines and Diagnost
; FILE REFERENCE: 2183-4646US
; CURRENT APPLICATION NUMBER: US/09/741,744A
; PRIOR FILING DATE: 2000-12-19
; PRIOR APPLICATION NUMBER: PCT/NL99/00377
; PRIOR FILING DATE: 1999-06-17
; NUMBER OF SEQ ID NOS: 148
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 134
; LENGTH: 15186
; TYPE: DNA
; ORGANISM: Newcastle disease virus LaSota
US-09-741-744A-134

Query Match 85.0%; Score 1412.4; DB 10; Length 15186;
Best Local Similarity 90.6%; Pred. No. 0;
Matches 1506; Conservative 0; Mismatches 156; Indels 0; Gaps 0;

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QY 1 ATGGGCTCCAGATCTTCTACAGGATCCAGTACCTCTGATGCTGACCGTCCGGGTGCG 60
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QY 61 CTGGCACTCAGTTGCGTCTGTCCGCAAGCTCCCTTGTATGGCAGGCTCTTTCAGGTGCA 120
Db 4604 CTGGTACTGAGTTGCATCTGTCCGCAAACTCCATGTATGGCAGGCTCTTTCAGGTGCA 4663
QY 121 GGAATTTGGTGTACAGAGCAAAAGCAGTCAACATATACACCTCATCTCAGACAGGCTCA 180
Db 4664 GGAATTTGGTGTACAGAGCAAAAGCAGTCAACATATACACCTCATCTCAGACAGGCTCA 4723
QY 181 ATCATAGTCAAGTTACTTCCCAATATGCCCAAGATAAAGAGCGGTGTGCAAAAGCCCCG 240
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Db 4724 ATCATAGTTAAGTCTCTCCGAAATCTGCCAAGATAGAGGAGCATGTGCGAAGGCCCCC 4783
QY 241 TTGAGGCGGTAAACAGGACATTTGACTATTTTGTCTCACCCTTTGGTGTATTTCTATTCGT 300
Db 4784 TTGGATGCATACAACAGGACATTTGACCACTTTGTCTCACCCTTTGGTGTATTCCTATCCGT 4843
QY 301 AGGATACAAGAGTCTGTGACTACATCTCGAGAGGAGGAAACAGGAGCGCTTTATAGGCGCC 360
Db 4844 AGGATACAAGAGTCTGTGACTACATCTGGAGGAGGAGACAGGCGCGCTTTATAGGCGCC 4903
QY 361 ATTATCGCGGTGCGAGTCTCGGGGTGCAACCGCTGCACAGATAACAGAGCACTTCGGCT 420
Db 4904 ATTATCGCGGTGCGCTCTTGGGGTGGCACTCGCGGACAAATTAACAGCGCGCGCAGCT 4963
QY 421 CTGATACAAGCAACCAAAATGCTCCCAACATCTCCCGCTTTAAAGAGAGAAATTTCTGCA 480
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QY 481 ACCAATGAGGCTGTGCAGAGGTCACTGATGATTTATCACAATAGCACTAGCACTGGCAGTTGG 540
Db 5024 ACCAATGAGGCTGTGCATGAGTCACTGACGGATTTATCGCACTAGCACTGGCAGTTGG 5083
QY 541 AAGATGCAAGCAATTTGTTAATGACCAATTTAATAAAACAGCTCAGCAATTTGGACTGTATA 600
Db 5084 AAGATGCAAGCAATTTGTTAATGACCAATTTAATAAAACAGCTCAGCAATTTAGACTGCATC 5143
QY 601 AAAATTAACAGAGGTTGGTGTAGAACTCAACCTGTATCTAACTGAAATTTGACTACAGTA 660
Db 5144 AAAATTTGACAGCAAGTTGGTGTAGAGTCAACCTGTATCTAACTGAAATTTGACTACAGTA 5203
QY 661 TTCGGGCGACAAATCACTTCCCTCCCTTAACCCAGCTGACTATCCAGCGCTTTTACAAAT 720
Db 5204 TTCGAGCACAAATCACTTCCCTGCTTTAAACAGCTGACTATTCAGGCACTTTTACAAAT 5263
QY 721 CTAGCTGTGGGAATATGGAATTAATTTGTAAGTGTAGGTAGGGAACCAACCACTC 780
Db 5264 CTAGCTGTGGGAATATGGAATTAATTTGTAAGTGTAGGTAGGGAACCAATCACTC 5323
QY 781 AGCTCATTAATTTGGTAGCGGCTGATCAACCGCAACCTTATTTCTGTAGCTCAAGACT 840
Db 5324 AGCTCATTAATTTGGTAGCGGCTTAAATCAACCGTAACCTTATTTCTGTAGCTCAAGACT 5383
QY 841 CAGCTCTTGGGTATACAGTAACTTACCTCAGTCGGGAACCTGAAATTAATTTGCTGTC 900
Db 5384 CAACCTCTTGGGTATACAGTAACTTACCTCAGTCGGGAACCTGAAATTAATTTGCTGTC 5443
QY 901 ACCTACTTTGGAAACCTTTGTCTGTAAAGTACAACCAAGGATTTGCTTCAGCACTTCGCCA 960
Db 5444 ACCTACTTTGGAAACCTTTATCCGTAAAGCAACCAAGGATTTGCTTCGSCACTTTGCC 5503
QY 961 AAGGTGGTGTGAAGGTGCGTTCGGTGTAGTAGAAGAACTTGACACCTCATCTGTATAGAG 1020
Db 5504 AAGGTGGTGTGAAGGTGCGTTCGGTGTAGTAGAAGAACTTGACACCTCATCTGTATAGAA 5563
QY 1021 ACCGATTTGGATCTATATTGTACAAGATAGTACATTCCTTATGCTCTCGTATTTAT 1080
Db 5564 ACTGACTTAGATTTATTTGTACAAGATAGTAACTGTTCCCTATGTTCCCTGTTATTTAT 5623
QY 1081 TCCTGTTTGAAGCGGCAATACATCGGCTTGCATGTACTCGAAGACTGAAGCGGCACTCACT 1140
Db 5624 TCCTGTTTGAAGCGGCAATACATCGGCTTGCATGTACTCGAAGACTGAAGCGGCACTCACT 5683
QY 1141 AGCGGTATACACTCTCAAGGCTCAGTTATTCGCACTGTAAAGTGAACATGACATGTAGA 1200
Db 5684 ACACATATACACTCTCAAGGCTCAGTTATTCGCACTGTAAAGTGAACATGACATGTAGA 5743
QY 1201 TGTGACAGCCCCCGGTTATCATATCGCAAAATTTATGGAGAGGCTGTGCTCTAATAGAT 1260
Db 5744 TGTGTAACCCCCCGGTTATCATATCGCAAAATTTATGGAGAGGCTGTGCTCTAATAGAT 5803
QY 1261 AGGCAATATGCAATGCTCTTATCTTTAGACGGAATAACTTTGAGGCTCAGTGGGAAATTT 1320
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Db 5804 AAACAAATCATCAATGTTTTTATCTTATAGGCGGGATAACTTTAAAGGCTCAGTGGGAATTC 5863
QY 1321 GATGCACTTATCAAAAGAAATATCTCAATACAAATCTCAAGTAATCTGTACACGGCAAT 1380
Db 5864 GATGTAACCTTATCAGAAGAAATATCTCAATACAAATCTCAAGTAATCTCAAGCAAT 5923
QY 1381 CTCGATATCTGACTGAGCTTTGGGAATGTCAACAACTCGATAAGTAAGTCTTTAGATAAG 1440
Db 5924 CTTGATATCTCACTGAGCTTTGGGAATGTCAACAACTCGATCAAGTAAGTCTTTAGATAAG 5983
QY 1441 TTAGAGAAACCAACAGCAAACTAGACAAAGTCAATGTCAAACTGACCAACATCCCGCT 1500
Db 5984 TTAGAGAAACCAACAGCAAACTAGACAAAGTCAATGTCAAACTGACCAACATCCCGCT 6043
QY 1501 CTCATCACCTATATCGTTTTTAACTGTCTATATCTCTTGTGTTGTTATAGCTGGTT 1560
Db 6044 CTCATTAAGCTATATCGTTTTTAACTGTCTATATCTCTTGTGTTGTTATAGCTGGTT 6103
QY 1561 CTAGCATCTACCTGATGTACAAGCAAAAGCGCAACAGAGACCTTGTATGCTTGG 1620
Db 6104 CTAGCATCTACCTAATGTACAAGCAAAAGCGCAACAGAGACCTTGTATGCTTGG 6163
QY 1621 AATAATACCTCGATCAGATGAGAGCCACTACGAAATGTGA 1662
Db 6164 AATAATACCTCGATCAGATGAGAGCCACTACGAAATGTGA 6205
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RESULT 6

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US-10-377-718-3
; Sequence 3, Application US/10377718
; Publication No. US20030175291A1
; GENERAL INFORMATION:
; APPLICANT: KUO, Tsun Yuang
; TITLE OF INVENTION: MULTIPLE AND MULTIVALENT DNA VACCINES IN OVO
; FILE REFERENCE: 39734-186920
; CURRENT APPLICATION NUMBER: US/10/377,718
; CURRENT FILING DATE: 2003-03-04
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 3
; TYPE: DNA
; LENGTH: 15186
; ORGANISM: Newcastle disease virus (NDV)
US-10-377-718-3
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Query Match 85.0%; Score 1412.4; DB 14; Length 15186;
Best Local Similarity 90.6%; Pred. No. 0;
Matches 1506; Conservative 0; Mismatches 156; Indels 0; Gaps 0;
QY 1 ATGGGCTCCAGATCTTCTACAGGATCCAGTACCTCTGATGCTGACCGTCCGGTCCGG 60
Db 4544 ATGGGCTCCAGATCTTCTACCAAGAACCCAGCACCTATGATGCTGACTATCGGGTGG 4603
QY 61 CTGGCACTGAGTTGGTCTGTCCGCAAGCTCCCTTGTATGGCAGGCTCTTGCAGCTGA 120
Db 4604 CTGGTACTGAGTTGCATCTGTCCGGCAAACTCCATGATGGCAGGCTCTTGCAGCTGA 4663
QY 121 GGGATTTGGTCAAGGAGACAAAGACTCAACATATACCTCATCTCAGACAGGTCA 180
Db 4664 GGAATTTGGTTACAGGAGACAAAGCCGTCAACATATACCTCATCTCAGACAGGTCA 4723
QY 181 ATCATAGTCAAGTTACTCCCAAAATATGCCAAAGATAAAGAGCGCTGTGCAAAAGCCCG 240
Db 4724 ATCATAGTTAAGTCTCTCCGAAATCTGCCAAGGATAAGGAGCATGTGCGAAAGCCCCC 4783
QY 241 TTGAGGCGGTCAACAGAGCAATTTGACTATTTGTCTACCCCTTTGGTGAATCTTATTCGT 300
Db 4784 TTGATGTCATACAACAGGACATTTGACCTTTTGTCTCACCCCTTTGGTGAATCTTATTCGT 4843
QY 301 AGGATACAAGAGTCTGTGACTACATCTCGAGAGGAGAAACAGGAGCGCTTATAGCGGCC 360
Db 4844 AGGATACAAGAGTCTGTGACTACATCTGAGAGGAGGAGACAGGAGCGCTTATAGCGGCC 4903
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361 ATTATCGCGGTGAGCTCTGGGGTTCACACCGCTGCACAGATAACAGCAGCTTCGGCT 420
Db |||||
4904 ATTAATTGGCGGTGGCTCTTGGGGTTCGCAACTGCGGCACAAATAACAGCGCGCGCAGCT 4963
Qy |||||
421 CTGATACAAGCCAAACCAAAATGCTCGCAACATCTCCGGCTTAAAGAGAGAAATTCGTGCA 480
Db |||||
4964 CTGATACAAGCCAAACCAAAATGCTCGCAACATCTCCGGCTTAAAGAGAGCAATTCGCGCA 5023
Qy |||||
481 ACCAATGAGGCTGTGACGAGGTCACTGATGGATATCAAACTAGCAGTGGCAGTTGGG 540
Db |||||
5024 ACCAATGAGGCTGTGACGAGGTCACTGACGGATATCGCAATTCGCAATTCGAGTGGCAGTTGGG 5083
Qy |||||
541 AAGATGACGCAATTTGTTAATGACCAAGTTAATAAAGCTCAGGAAATTCGAGTGGATATGATA 600
Db |||||
5084 AAGATGACGCAATTTGTTAATGACCAATTTAATAAAGCTCAGGAAATTCGAGTGGATATGATA 5143
Qy |||||
601 AAAATATCCAGCAGGTTGGTGTAGAACTCAACCTGTATCTAATGAATGACTACAGTA 660
Db |||||
5144 AAAATTCACAGCAAGTTGGTGTAGAGCTCAACCTGTACCTAACCGAATTCAGTACAGTA 5203
Qy |||||
661 TTGGGGCCAAATCACTTCCCTGCCCTTAACCCAGCTGACTATCCAGGGCTTTCAAT 720
Db |||||
5204 TTGGGGCCAAATCACTTCCCTGCCCTTTAAACAAGCTGACTATTCAGGCACCTTTCAAT 5263
Qy |||||
721 CTAGCTGGTGGGAATATGGATTAATCTGTGACTAAGTTAGGTAGGGAACAACCAACTC 780
Db |||||
5264 CTAGCTGGTGGGAATATGGATTAATCTGTGACTAAGTTAGGTAGGGAACAATCAACTC 5323
Qy |||||
781 AGCTCAATTAATGGTAGCGCTGATCACCGGCAACCTATTTCTGTACGACTCACAGACT 840
Db |||||
5324 AGCTCAATTAATGGTAGCGCTTAATCACCGGTAACCTATTTCTATACGACTCACAGACT 5383
Qy |||||
841 CAGCTCTTGGGTATACAGGTAAACCTACCTCAGTCCGGAACTGAATATATGCGTGCC 900
Db |||||
5384 CAACTCTTGGGTATACAGGTAACTCTACCTTCACTCGGGAACCTAAATTAATATGCGTGCC 5443
Qy |||||
901 ACCTACTTGAACACTTGTCTGTAAGTACAAACAAAGATTTGCTCAGCACTCGTCCCA 960
Db |||||
5444 ACCTACTTGAACACTTATCGTGAAGCAACACAGGGGATTTGCTCGGCACCTTGTCCCC 5503
Qy |||||
961 AAGTGGTGTATGAGGTGCGTTCGGTGTATGATGAAGAACTTGACACCTCATACTGTATAGAG 1020
Db |||||
5504 AAGTGGTGTACAGAGTTCGGTTCGTGTATGATGAAGAACTTGACACCTCATACTGTATAGAA 5563
Qy |||||
1021 ACCGATTTGATCTATATTTGTAAGAATATGATGACATTCCTGTATGCTCCTGTGATTTAT 1080
Db |||||
5564 ACTGACTTATGATTTATATTTGTAAGAATATGATGACATTCCTGTATGCTCCTGTGATTTAT 5623
Qy |||||
1081 TCCTGTTTGAAGCGCAATACATCGGCTTGATGTACTCGAAGACTGAAGCGCACTCACT 1140
Db |||||
5624 TCCTGTTTGAAGCGCAATACATCGGCTTGATGTACTCGAAGCGCAAGCGCACTTACT 5683
Qy |||||
1141 ACGCGGTATCATGACTCTCAAGGCTCAGTTTATGCGCAACTGTAAAGATGACAACTGATAGA 1200
Db |||||
5684 ACACCATACATGACTATCAAGGTTTCACTCATGCCAACTGCAAGATGACAACTGATAGA 5743
Qy |||||
1201 TGTGCAAGACCCCGGTATCATATCGCAAAATATGGAAGAGTGTCTCTAAATAGAT 1260
Db |||||
5744 TGTGTAACCCCGGGGTATCATATCGCAAACTATGGAAGAGCGGTCTCTAAATAGAT 5803
Qy |||||
1261 AGGCAATCATGCAATGCTCTATCCTTAGACGGAATTAATTTGAGGCTCAGTGGGAATTT 1320
Db |||||
5804 AACAATCATGCAATGTTTATCCTTAGCGGGATTAATTTAAGGCTCAGTGGGAATTC 5863
Qy |||||
1321 GATGCAATTTATCAAAAGAAATATCTCAATAAAGATTTCTCAAGTAATTCGTGACAGGCAAT 1380
Db |||||
5864 GATGTAATTTATCAGAAGAAATATCTCAATACAAGATTTCTCAAGTAATTAATAACAGGCAAT 5923
Qy |||||
1381 CTGATATCTCGACTGAGCTTGGAAATGTCAACTCGATAGTAATGCTTTAGATAAG 1440
Db |||||
5924 CTTGATATCTCAACTGAGCTTGGAAATGTCAACTCGATAGTAATGCTTTGATAAG 5983
Qy |||||
1441 TTAGAGGAAGCAACAGCAAACTAGACAAGGTCAATGTCAAACTGACCAGCACATCGCT 1500

5984 TTAGAGGAAGCAACAGCAAACTAGACAAGTCAATGTCAAACTGACTAGCACATCTGCT 6043
Qy |||||
1501 CTATCACCTATATCGGTTTAACTGTATATCTCTTGTGTGTATACTTAGCTGTGTT 1560
Db |||||
6044 CTCAATACCTATATCGGTTTGAAGTATATATCTCTTGTGTGTATACTTAGCTGTGTT 6103
Qy |||||
1561 CTAGCATGCTACCTGTATGATCAAGCAAAAGCGCAACAGAGACCTTGTGTATGCTTGGG 1620
Db |||||
6104 CTAGCATGCTACCTGTATGATCAAGCAAAAGCGCAACAAAGACCTTATATGCTTGGG 6163
Qy |||||
1621 AATAATACTCTAGATCAGATGAGGACCACTACGAAATATGTA 1662
Db |||||
6164 AATAATACTCTAGATCAGATGAGGACCACTACGAAATATGTA 6205

RESULT 7
US-10-429-735-3
; Sequence 3, Application US/10429735
; Publication No. US20030207836A1
; GENERAL INFORMATION:
; APPLICANT: KUO, Tsun Yuan
; TITLE OF INVENTION: VACCINE ACCELERATOR FACTOR (VAF) FOR IMPROVEMENT OF VACCINATIONS
; FILE REFERENCE: 39734-188449
; CURRENT APPLICATION NUMBER: US/10/429, 735
; CURRENT FILING DATE: 2003-05-06
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 3
; LENGTH: 15186
; TYPE: DNA
; ORGANISM: Newcastle disease virus (NDV)
US-10-429-735-3

Query Match 85.0%; Score 1412.4; DB 15; Length 15186;
Best Local Similarity 90.6%; Pred. No. 0;
Matches 1506; Conservative 0; Mismatches 156; Indels 0; Gaps 0;

Qy 1 ATGGGCTCCAGATCTTCTACAGGATCCCAAGTACCTCTGATGCTGACCGTCCGGGTGCGG 60
Db |||||
4544 ATGGGCTCCAGATCTTCTACAGGATCCCAAGTACCTCTGATGCTGACCTATGCTATCCGGGTGCG 4603
Qy 61 CTGGCACTGATGTCGGTCTGTCGCAAGAGTCCCTTGTATGCGAGGCTCTTTGACAGTGA 120
Db |||||
4604 CTGGTACTGATGTCGATCTGTCGGCAAACTCCATTGATGCGAGGCTCTTTGACAGTGA 4663
Qy 121 GGGATTGTGTGACAGGAGCAAGAGTCAACATATACACCTCATCTCAGACAGGTC 180
Db |||||
4664 GGAATTGTGTGACAGGAGCAAGGCTCAACATATACACCTCATCTCAGACAGGATCA 4723
Qy 181 ATCATAGTCAAGTACTTCCCAAAATATGCCCAAGATAAGAGGCGTGTGCAAAAGCCCCG 240
Db |||||
4724 ATCATAGTCAAGTACTTCCCGAATTCGCCCAAGATAAGAGGAGCATGTGCAAAAGCCCC 4783
Qy 241 TTGGAGCGGTACAAAGAGCAATTCATCTTTGCTACCCCTTGTGTGATTTCTATTCGT 300
Db |||||
4784 TTGGATGTCATACAAAGAGCAATTCATCTTTGCTACCCCTTGTGTGATTTCTATTCGT 4843
Qy 301 AGGATACAGAGTCTGTGACTACATCTGGAGGAGGGAACAGGAGCGCTTATAGCGCC 360
Db |||||
4844 AGGATACAGAGTCTGTGACTACATCTGGAGGAGGAGAGAGGCGGCTTATAGCGCC 4903
Qy 361 ATTATCGCGGTGACGCTCTCGGGTTGCAACCGCTGCACAGATAACAGCAGCTTCGGCT 420
Db |||||
4904 ATTATCGCGGTGCTGCTCTTGGGTTGCACTGCGCAAAATACAGCGCGCGCAGCT 4963
Qy 421 CTGATACAGCGCAACCAAAATGCTGCCAATCTCTCGGCTTAAAGAGAGAAATTCGTGA 480
Db |||||
4964 CTGATACAGCGCAACCAAAATGCTGCCAATCTCTCGGCTTAAAGAGAGCAATTCGCGCA 5023
Qy 481 ACCAATGAGGCTGTGACAGGCTCACTGATGATATCACTAGCAGTGGAGTTGGG 540

Db 5024 ACCAATGAGGCTGTGCATGAGGTCACTGACGGATTATCGCACTAGCAGTGGCAGTTGGG 5083
Qy 541 AAGATGCGAGCAATTTGTTAATGACCAAGTTTAAATAAACAAGCTCAGGAATGGACCTGTATA 600
Db 5084 AAGATGCGAGCAATTTGTTAATGACCAATTTAATAAACAAGCTCAGGAATGGACCTGTATA 6205
Qy 601 AAAAATACCCAGCAGTGGTGTAGAACTCAACCTGTATCTAACTGAATTCAGTACAGTA 660
Db 5144 AAAATGACAGCAAGTGGTGTAGAGCTCAACCTGTATCTAACTGAATTCAGTACAGTA 5203
Qy 661 TTCGGGCCACAAATCACATTCGCCCTGCCCTAACCCAGCTGACTATCCAGCGCTTTTACAA 720
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Qy 721 CTAGCTGTGGGAATATCGAATTAATCTTTGTTAGTAACTAGTGTAGGTAGGGAAACCAACATC 780
Db 5264 CTAGCTGTGGGAATATCGAATTAATCTTTGTTAGTAACTAGTGTAGGTAGGGAAACCAACATC 5323
Qy 781 AGCTCAATTAATTTGGTGTAGCGGCTGTATCACCGGCAACCTTATTCGTAGCACTCAGACT 840
Db 5324 AGCTCAATTAATCGGTGTAGCGGCTTAATCACCGGTAACCTTATTCGTAGCACTCAGACT 5383
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Db 5384 CAACCTTTGGGTATACAGTAACCTTACCTCAGTGGGAACTTGAATTAATATGCGTCC 5443
Qy 901 ACCTACTTTGGAACCTTGTGTAGTACCAACCAAGGATTTGCTCAGCACTCGTCCCA 960
Db 5444 ACCTACTTTGGAACCTTGTGTAGTACCAACCAAGGATTTGCTCAGCACTCGTCCCA 5503
Qy 961 AAGGTGGTGTATGAAAGTGGTTCGGTGTAGTAAAGAACTTGACACCTCATCTGTATAGAG 1020
Db 5504 AAGGTGGTGTATGAAAGTGGTTCGGTGTAGTAAAGAACTTGACACCTCATCTGTATAGAG 5563
Qy 1021 ACCGATTTGGATCTAATTTGTACAAAGATAGTGAATTCCTTATCTCTCGTGTATTTAT 1080
Db 5564 ACTGACTTAGATTTTATTTGTACAAAGATAGTGAATTCCTTATCTCTCGTGTATTTAT 5623
Qy 1081 TCCTGTTTGGGCGCAATACATCGCTTGCATGTACTCGAAGCTGGAAGCGCACTCACT 1140
Db 5624 TCCTGTTTGGGCGCAATACATCGCTTGCATGTACTCGAAGCTGGAAGCGCACTCACT 5683
Qy 1141 ACGCGGTATCATGACTCTCAAGGCTCAGTTATTTGCCAACTGTAAGATGACAACTGTAGA 1200
Db 5684 ACACCATATCATGACTCATCAAGGCTCAGTATCGCCAACTGCAAGATGACAACTGTAGA 5743
Qy 1201 TGTGAGACCCCGGGTATCATATCGCAAAATTAAGAGAGCTGTGTCTTAATAGAT 1260
Db 5744 TGTGTAACCCCGGGTATCATATCGCAAAATTAAGAGAGCTGTGTCTTAATAGAT 5803
Qy 1261 AGGCAATCATGCAATGCTCTATCTTATGACGGAATACTTTGAGGCTCAGTGGGAATTT 1320
Db 5804 AAACAATCATGCAATGCTCTTATCTTATGAGGGAATACTTTAAGGCTCAGTGGGAATTT 5863
Qy 1321 GATGCAACTTATCAAAAAGATATCTCAATACAGATTTCTCAAGTAATCGTGACAGGCAAT 1380
Db 5864 GATGTAACCTTATCAGAGAAATATCTCAATACAGATTTCTCAAGTAATTAATAAGCAAT 5923
Qy 1381 CTCGATATCTGACTGAGCTGGGAATGTCAACAACTCGATGAAGTAAGTCTTTAGATAG 1440
Db 5924 CTTGATATCTCAACTGAGCTGGGAATGTCAACAACTCGATGAAGTAAGTCTTTAGATAG 5983
Qy 1441 TTAGAGGAAGCAACAGCAAACTAGACAGGTCAATGTCAAACTGACAGCACTCCGCT 1500
Db 5984 TTAGAGGAAGCAACAGCAAACTAGACAGGTCAATGTCAAACTGACAGCACTCCGCT 6043
Qy 1501 CTCATCACTATCTGTTTAACTGTCAATATCTCTGTTTGTGGTATCTTACCTGCTGTT 1560
Db 6044 CTCATCACTATCTGTTTAACTGTCAATATCTCTGTTTGTGGTATCTTACCTGCTGTT 6103
Qy 1561 CTAGCATGCTACTGATGTACAGCAAAAGGCGCAACAGAGCACTTTGTTATGCGTGGG 1620
Db 6104 CTAGCATGCTACTGATGTACAGCAAAAGGCGCAACAGAGCACTTTGTTATGCGTGGG 6163

Qy 1621 AATAATACCTCGATCAGATGAGAGCCACCTACGAAATGTGA 1662
Db 6164 AATAATACCTTAGATCAGATGAGAGCCACCTACGAAATGTGA 6205

RESULT 8

US-09-881-457A-1
; Sequence 1, Application US/09881457A
; Patent No. US20020081316A1
; GENERAL INFORMATION:
; APPLICANT: Cochran, Mark D
; APPLICANT: Cook, Stephanie M
; APPLICANT: Wild, Martha A
; TITLE OF INVENTION: No. US20020081316A1el Avian Herpes Virus and Uses Thereof
; FILE REFERENCE: SY01105K1QKQK
; CURRENT APPLICATION NUMBER: US/09/881.457A
; CURRENT FILING DATE: 2001-06-14
; PRIOR APPLICATION NUMBER: 09/426,352
; PRIOR FILING DATE: 1999-10-25
; PRIOR APPLICATION NUMBER: 08/804,372
; PRIOR FILING DATE: 1997-02-21
; PRIOR APPLICATION NUMBER: PCT/US95/10245
; PRIOR FILING DATE: 1995-08-09
; PRIOR APPLICATION NUMBER: 08/663,566
; PRIOR FILING DATE: 1996-06-13
; PRIOR APPLICATION NUMBER: 08/288,065
; PRIOR FILING DATE: 1994-08-09
; PRIOR APPLICATION NUMBER: PCT/US93/05681
; PRIOR FILING DATE: 1993-06-14
; PRIOR APPLICATION NUMBER: 08/023,610
; PRIOR FILING DATE: 1993-02-26
; PRIOR APPLICATION NUMBER: 07/898,087
; PRIOR FILING DATE: 1992-06-12
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 3570
; TYPE: DNA
; ORGANISM: Newcastle disease virus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1194)..(2888)
; OTHER INFORMATION: NDV Fusion Protein
; NAME/KEY: misc feature
; LOCATION: (1355)
; OTHER INFORMATION: n = any nucleotide
US-09-881-457A-1

Query Match 82.8%; Score 1375.4; DB 9; Length 3570;
Best Local Similarity 90.4%; Pred. No. 0;
Matches 1502; Conservative 0; Mismatches 157; Indels 3; Gaps 3;
Qy 1 ATGGGCTCCAGATCTTCTACAGGATCCAGTACTCTGTAGTCTGACCTCGGGTCCGG 60
Db 1230 ATGGGCTCCAGATCTTCTACCAAGAACCCAGCACCTATGCTGCTACTATCCGGTCCGG 1289
Qy 61 CTGGCACTGAGTGGTCTGTCCGACAGCTCCCTTGTATGGAGGCTCTTGCAGCTCA 120
Db 1290 CTGGTACTGAGTGGTCTGTCCGCAAACTCCATTTGATGGAGGCTCTTGCAGCTCA 1349
Qy 121 GGGATTGTGGTGACAGGAGACAAAGCAGTCAACATATACCTCATCTCAGACAGGGTCA 180
Db 1350 -GGACTNTGGTTACAGGAGACAAAGCAATCAACATATACCTCATCTCAGACAGCA 1407
Qy 181 ATCATAGTCAAGTACTCCAAATATGCCAAAGATAAGAGGCGGTGTGCAAAAGCCCG 240
Db 1408 ATCATA-TTAAAGTCTCTCCCGAATCTGCCAAAGGATAAGAGGCGCATGTGCGAAAGCCCG 1466
Qy 241 TTGAGGGCGTCAACAGGACATTTGACTACTTTTGTCTACCCCTTGGTGTATTTCTTCT 300
Db 1467 TTGGATGATACACAGAGCACTTGTACCATTTGTCTACCCCTTGGTGTATTTCTTCT 1526


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QY 392 CCGCTGCACATACACGAGCTTCGGCTCTGATACAGCCCAACCAAAATGCTGCCACA 451
Db 5433 CAGCTGCACAAATACCCGAGCTGTAGCAATAGTAAAAAGCCAAATGCAAAATGCTGGCGA 5492
QY 452 TCCTCCGGCTTAAAGAGAGAATTTGTGCAACCAATGAGGCTGTGCACGAGGTCACTGATG 511
Db 5493 TAAACAATCTTCAATCTCAATTCATCCACCAAGCAGATCCGATGTGATACTG 5552
QY 512 GATTATCAACATAGCAGTGGAGATGGAGAGATCGACGAATTTGTTAATGACCAAGTTTA 571
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QY 572 ATAAACAGCTCAGGAATTTGACTGTATATAAAATTTACCAGCAGGTTCGGTAGAATCA 631
Db 5613 TCAACGGGATACATCTGCATCATCCGCTGCCATGATGCAATTTGGGTCAATTTAA 5672
QY 632 ACCTGTATCTAAGTAAATGACTACAGTATTTGGGCCCAAAATCACTTCCCTGCTCTAA 691
Db 5673 ATTTGTATCTCACTGAGCTTACTACAATATTTCAATCAAAATCAAAACCCCTGGCTGA 5732
QY 692 CCCAGCTCACTATCCAGGGCTTTACAATCTAGCTGGTGGGAATGGAATTAATTTGTTGA 751
Db 5733 CACCACCTTTCCATCCAAGC-TTTAAGAAATCCTCTCGGTAGCACCTTCCCAATTTGTCAT 5791
QY 752 CTAAGTTAGTGTAGGGAACCAACCACTCAGCTCA-TTAAATTTGGTAGCGGCTGATCAC 810
Db 5792 GAATCCAACTCAACACAAACTCAACACAGCAGAGTGTCTAGTAGGAGTGTAACT 5851
QY 811 GGCAACCCCTATTTCTGACGACTCACAGACTCAGCTCTTTGGGTATACAGTAACCCATCC 870
Db 5852 GGTCAAAATTTTCCATTTCCCAATGTACATGCAATGCTAAATTTCAATCAATGTTCCG 5911
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QY 1051 GTGACATTCCTATGCTCTCTGTTATTTATCTCTTTGAGCGGCAATACATCGGCTTGC 1110
Db 6092 GAGGTTCCCGATCCCTGAATCACAATATCAATGCTTTAAGGGGGAATCTTAATTTCTTGC 6151
QY 1111 ATGTACTGGAAGACTGAAGGGCACTCACTACGCGGTATACATGACTCTCAAAGGCTTCAGT 1170
Db 6152 ACTTTTACCCCTATTTATCGGAACTTTCTCAAGCGATTTGCAATTTGCCAATGGTGTGCT 6211
QY 1171 ATTGCCAACTGTAAAGATGACAACTGTAGATGTGACACCCCGGGTATCATATCGCAA 1230
Db 6212 TATGCCAACTGCAAACTTTTGTATGTAGTGTGCGGACCTTCCCATGTTGTGTCTCAA 6271
QY 1231 AATTATGAGAGCTGTGTCTTAATAGATAGGCAATCATGCAATGTCTATCTCTTAGAC 1290
Db 6272 GATGACAAACCAAGGATCAGCAATATGATATTAAGAGGTGTCTGAGATGATGCTTAGAC 6331
QY 1291 GGAATTAATTTGAGGCTCAGTGGGAATTTGATGCAACTTATCAAAGAATATCTCAATA 1350
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QY 1351 CAGATTTCTAAGTAAATGTGACAGGCAATCTGATATCTCGACTGAGCTGGGAATGTC 1410
Db 6392 ATTAATGCAAAATTTGTACATCTAAGTCTCTAGACTTTGTCAAAATCAAAATCAATA 6451
QY 1411 AACCAACTCGATAAGTAATGCTTTAGATAAGTTAGAGGAAAGCAAC 1455
Db 6452 AACAAATCTTTAAAGTGTGAGGATTTGGATTGAGATAGCAAC 6496
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RESULT 10
US-09-733-692A-62
; Sequence 62, Application US/09733692A
; Patent No. US20020155581A1
; GENERAL INFORMATION:
; APPLICANT: Murphy, Brian R.
; APPLICANT: Collins, Peter L.
; APPLICANT: Schmidt, Alexander C.
; APPLICANT: Durbin, Anna P.
; APPLICANT: Skiadopoulos, Mario H.
; APPLICANT: Tao, Tao
; TITLE OF INVENTION: USE OF RECOMBINANT PARAINFLUENZA VIRUSES (PIVs) AS
; TITLE OF INVENTION: VECTORS TO PROTECT AGAINST INFECTION AND DISEASE CAUSED
; TITLE OF INVENTION: BY PIV AND OTHER HUMAN PATHOGENS
; FILE REFERENCE: 15280-404100US
; CURRENT APPLICATION NUMBER: US/09/733.692A
; CURRENT FILING DATE: 2000-12-08
; PRIOR APPLICATION NUMBER: 60/170,195
; PRIOR FILING DATE: 1999-12-10
; NUMBER OF SEQ ID NOS: 62
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 62
; LENGTH: 15492
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Sequence of
; OTHER INFORMATION: pPLC.PIV32CT, 15474 bp in sense orientation
US-09-733-692A-62
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Query Match          9.8%; Score 162.2; DB 9; Length 15492;
Best Local Similarity 46.4%; Pred No. 4.9e-40;
Matches 634; Conservative 0; Mismatches 723; Indels 8; Gaps 3;

QY 92 CCCTTGATGGCAGGCTCTTGCAGCTGCAGGATTTGGTGACAGGAGTTCCTTCAATCAAAAGATCACTCA 5198
Db 5139 CCAITGCTGGAGATCAACTCCTCAATGTAGGGTCATTCAATCAAAAGATCACTCA 5198
QY 152 ACATATACACCTCATCTCAGACAGGTCAATCATAGTCAAGTACTTCCCAATATGCCCA 211
Db 5199 TGTACTACACTGATGGTGGCGCTAGCTTTATTTGTTGAAAATTTACTCCCAATCTTCCCC 5258
QY 212 AAGATAAAGAGCGGTGTGCAAAAGCCCGTTGGAGCGGTACAAACAGGACATTTGACTACT 271
Db 5259 CAAGCAATGGAACATGCAACATCACCAGTCTAGATGCATATAATGTTACCTTATTTAAGT 5318
QY 272 TGCTCACCCCTTGGTGATTTCTATTCTGATGATACAAAGATCTGTGACTACATCTGGAG 331
Db 5319 TGCTAACACCCCTGATTTGGAACCTGAGCAAAATTT-----TCTGCTGTTACAGATACCA 5372
QY 332 GAGGGAACAGGAGCGCTTATAGCGCCATTATCGCGGTGACGCTCTCGGGTTGCAA 391
Db 5373 AACCCCGCGAGAACGATTTCCAGAGTCTGTTATTTGGGCTTGTCTGCTAGGATGCTA 5432
QY 392 CCGCTGCACAGATAACAGCAGCTTCGGCTCTGATACAAAGCCCAACCAAAATGCTGCCACA 451
Db 5433 CAGCTGCACAAATAACCCGAGCTGTAGCAATAGTAAAGCCCAATGCAATGCTGTGCGA 5492
QY 452 TCCTCCGGCTTAAAGAGAGAATTTGTCGAACCAATGAGGCTGTGCAAGAGGTCACTGATG 511
Db 5493 TAAACAATCTTGCATCTTCAATTTCAATCCACCAACAGGAGTATCCGATGTGTAACCTG 5552
QY 512 GATTATCACACTAGCAGTGGCAGTTGGGAAGATGCAAGAAATTTGTTAATGACCAAGTTTA 571
Db 5553 CATCAAGAACAAATTTGCAACCCGAGTTCAAGCGATTCAGGATTCAGATCAATCAATGAGCAATG 5612
QY 572 ATAAACAGCTCAGGAATTTGGAATGTATATAAAATTTACCAGCAGGTTCGGTGTAGAACTCA 631
Db 5613 TCAACGGGATAACATCTGCATCATGCTGCCATGATGATGCACTAATTTGGTCAATATTTAA 5672
QY 632 ACCTGTATCTAAGTAAATTTGACTACAGTATTTGGGCCCAAAATCACTTCCCTGCTCTAA 691
```

5673 ATTGTATCTCACTGAGCTTACTAATAATTTTCATATCAATCAATCAAAACCTCGCTGA 5732
Db
QY 692 CCAGCTGACTATCCAGCGCTTTACAACTAGCTAGTGGGAAATGGAATTTACTTTGA 751
Db
5733 CACCACCTTTCCATCAAGC-TTTAAGAAATCTCTCGGTAGCAGCTTGGCAATTTGTCATT 5791
QY 752 CTAAGTTAGGTAGGAGAAACCAACTCAGCTCA-TTAAATTTGTAGCGGCTGATCAAC 810
Db
5792 GAATCCAACTCAACAACTCAACAGAGAGCTGCTCAGTAGCGGACTTTAACT 5851
QY 811 GGCAACCTATTTCTGTAGACTACAGACTCAGCTCTTTGGGTATACAGGTAACCTTACC 870
Db
5852 GGTCAATAATTTCCATTTCCCAATGTACATGCAAAATGCTAAATCAAAATTTCCG 5911
QY 871 TCAGTCGGGACCTGAATAATATGCGTGCACCTACTTTGAAACCTTGTCTGTAAGTACA 930
Db
5912 ACATTTAATATGCAACCCGGTGCAGGTAATTTGATCTAATTTGATCTCTCTGCAAAACCAT 5971
QY 931 ACCAAAGGATTTGCTCAGCACTCGTCCCAAGGTGGTATGAAGGTGGTTCGCTGATA 990
Db
5972 AATTTCAAGAGTAGTTGTACAGTTCTTAATAGAAATTTAGAAATATGCAATGAACATA 6031
QY 991 GAGAACTTGACACTCATCTGATAGAGACCGAATTTGGATCTATATTTGTACAGAAATA 1050
Db
6032 CAAAACCTACCAGCAATGATTTGCTGTACACCAAACTCTGTATTTTGTAGATCAAT 6091
QY 1051 GTGACATTCCTATGCTCTCGTATTTATTTCTGTTTGGCGGCAATATCATCGGCTTGC 1110
Db
6092 GAGGTTCCCGGATCCCTGAATCAAAATATCAATGCTTAAAGGGGAAATCTTAATTTCTTGC 6151
QY 1111 ATGTACTCGAAGACTGAAGCGCACTCACTACGCGGTACATGACTCTCAAGGCTCAGTT 1170
Db
6152 ACTTTACCCCTATTATTCGGGAATTTCTCAAGGATTTGCAATTTGCTGCTC 6211
QY 1171 ATTGCCAACTGTAGATGACAACTAGATGATGAGAGAGAGAGAGAGAGAGAGAGAGAG 1230
Db
6212 TATGCCAACTGCAAACTTTTGTGATGTAAGTGTGCGGACCTCCCATTTGTTGCTCAA 6271
QY 1231 AATATGGAAGCTGTCTCTAATAGATAGGCAATCATGCAATGCTTATCGTTAGAC 1290
Db
6272 GATGACAAACAGGATCAGCAATTAATGATTAAGAGGTGCTCTGAGATGATGCTTGAC 6331
QY 1291 GGAATAACTTTGAGGCTCAGTGGGAAATTTGATGCAACTTTATCAAAAGAAATATCTCAATA 1350
Db
6332 ACTTTTCATTTAGATCACTATCAATCAATGCTACATAGCTGACAGACTTCTCAATG 6391
QY 1351 CAGAACTTCAAGTATGCTGACAGGCAATCTCGATATCTCGACTGAGCTTGGGAATGTC 1410
Db
6392 ATTAATGCAAAATATTTGATCATCTAAGTCTCTAGACTTTGCAAAATCAAAATCAATCAATA 6451
QY 1411 AACAACTCGATAAGTAAATGCTTTAGATAAGTTAGAGGAAAGCAAC 1455
Db
6452 AACAAATCTTTAAAGTGTGAGGATTTGATTTGAGATAGCAAC 6496

RESULT 11

US-09-733-692A-61
; Sequence 61, Application US/09733692A
; Patent No. US20020155581A1
; GENERAL INFORMATION:
; APPLICANT: Murphy, Brian R.
; APPLICANT: Collins, Peter L.
; APPLICANT: Schmidt, Alexander C.
; APPLICANT: Durbin, Anna P.
; APPLICANT: Skladopoulos, Mario H.
; APPLICANT: Tao, Tao
; TITLE OF INVENTION: USE OF RECOMBINANT PARAINFLUENZA VIRUSES (PIVs) AS
; TITLE OF INVENTION: VECTORS TO PROTECT AGAINST INFECTION AND DISEASE CAUSED
; TITLE OF INVENTION: BY PIV AND OTHER HUMAN PATHOGENS
; FILE REFERENCE: 15280-404100US
; CURRENT APPLICATION NUMBER: US/09/733,692A
; CURRENT FILING DATE: 2000-12-08
; PRIOR APPLICATION NUMBER: 60/170,195

; PRIOR FILING DATE: 1999-12-10
; NUMBER OF SEQ ID NOS: 62
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 61
; LENGTH: 15498
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Sequence of
; OTHER INFORMATION: pFLC.PIV32TM, 15498 bp in sense orientation
US-09-733-692A-61

Query Match 9.8%; Score 162.2; DB 9; Length 15498;
Best Local Similarity 46.4%; Pred. No. 4.9e-40;
Matches 634; Conservative 0; Mismatches 723; Indels 8; Gaps 3;
QY 92 CCCTTGATGTGAGGAGGCTTTGCGAGCTGCGAGGATTTGGTGACAGGAGAGCAAAAGCAGTCA 151
Db
5136 CCATTGCTGGAGATCAACTCTCTCAATGTAGGGTCAATCAATCAAGATAGATCACTCA 5195
QY 152 ACATATACACTCATCTATTCAGACAGGGTCAATCATAGTCAAGTTACTCCCAATAATGCCCA 211
Db
5196 TGTACTACACTGATGGTGGCGCTAGCTTTATTTGTTGTAAATTTACTACCAATCTTCCCC 5255
QY 212 AAGATAAGAGGCGTGTGCAAAAGCCCCGTTGGAGGCTTACACAGGACATTTGACTACTT 271
Db
5256 CAAGCAATGGAACATGCAACATCACCAGTCTAGATGCATATAATGTTACCCCTATTTAAGT 5315
QY 272 TGCTCAACCCCTTTGTTGATTTCTATTCTGATAGGATACAAGAGTCTGTGACTACATCTGGAG 331
Db
5316 TGCTAACCCTCTGATTTGAACTCTGAGCAAAATTT-----TCTGCTTTACAGATACCA 5369
QY 332 GAGGAAACAGGAGCGCTTTATAGCGCCATTAATGCGCGTGCAGCTCTCGGGTTGCAA 391
Db
5370 AACCCGCGCGAGAACGATTTGCGAGGATCGTTATTTGGGCTTGTGCACTAGGAGTAGCTA 5429
QY 392 CCCTCAGACAGATAACAGCAGCTTCGGCTCTGTATACAAGCCACCAAAATTTGTTAAACAGCTTA 451
Db
5430 CAGCTGCACAAATAACCGCAGCTGTAGCAATAGTAAAGCCAAATGCAAAATGCTGCTGCGA 5489
QY 452 TCCTCGGCTTAAAGAGAGAAATTTGCTCAACCAATGAGGCTGTGCGAGGCTCACTGATG 511
Db
5490 TAAACAATCTTGTGATCTTCAATTCATCCACCAAGGAGTATCGATGTGATAGTCTG 5549
QY 512 GATTATCAAACTAGCAGTGGCGAGTTGGGAAGATGACAGCAATTTGTTAAACAGCTTTA 571
Db
5550 CATCAAGAACAAATTTGCAACCGCAGTTCAAGCGATTCAGGATCATCAATCAATGGAGCCATTG 5609
QY 572 ATAAACAGCTCAGGAATTTGGAATGATATAAAATTTACCCAGCAGGTTGGTGTAGAACTCA 631
Db
5610 TCAACGGGATAACATCTGCAATCATGCGGTGCCCATGATGCACTAATTTGGGTCAATATA 5669
QY 632 ACCTGTATCTTAAGTAAATTTGACTACAGTATTTGGGGCCACAAATCACTTCCCTCCCTTAA 691
Db
5670 ATTTGATCTCACTGAGCTTACTCAATATTTCAATCAATCAAAACCTTCGCGCTGA 5729
QY 692 CCAGCTGACTATCCAGGCGCTTTCAATCTAGCTGGTGGGAATATGGATTTACTTGTGA 751
Db
5730 CACCCTTTCCATCCCAAGC-TTTAAGAAATCTCTCGGTAGCAGCTTGGCAATTTGCTAAT 5788
QY 752 CTAAAGTTAGGTGATAGGGAACCAACTCAGCTCA-TTAAATTTGGTAGCGGCTGATCACC 810
Db
5789 GAATCCAACTCAACCAAACTCAACAGCAGAGCTGCTCAGTAGCGGACTGTTTAACT 5848
QY 811 GGCAACCTTATTTGTACGACTCAGACTCTGCGGTATACAGGTAACCTTACCC 870
Db
5849 GGTCAAAATTTTCCATTTTCCCAATTTGATACATGCAATGCAATGCAATCAATGTTCCG 5908
QY 871 TCAGTCGGGAACCTGAATTAATATGCGTGCACCTACTTGGAAACCTTTGTTGTAGTACA 930
Db
5909 ACATTTATAATGCAACCCCGTGCAGAGGTAATTTGATCTAATTTGCTATCTCTGCAAAACCAT 5968
QY 931 ACCAAAGGATTTGCTCAGCACTCTGCTCCCAAGGTTGATGAGGTCGTTCCGTTGATA 990

Db 5969 AAATTACAGAGTAGTGTGTAACAAGTCTCTTAATAGAAATTCAGAAATGCAAACTA 6028
QY 991 GAAGAACTTGACACTCTATCTGTATAGAGACCGAATTTGGATCTTAATTTGACAGAAATA 1050
Db 6029 CAAAATACCCAGGCAATGATTTGTTTCGTGACACCAAACTCTGTATTTTGTAGATACAA 6088
QY 1051 GTGACATTCCTGTATGCTCTGCTGTTATTTATTCCTGTTTGGAGGCAATACATCGCTTGC 1110
Db 6089 GAGGTTCCCGGATCCCTGGAATCAAAATCAATATCAATGCTTTAAGGGGAATCTTAATTCCTTC 6148
QY 1111 ATGTACTCGAAGACTGAAGGGCACTCACTAGCGCGTACATGACTCTCAAAGGCTCAGTT 1170
Db 6149 ACTTTTACCCCTATTTATCGGAACTTTCTCAAGCGATTCGCAATTTGGCAATGGTGTGCTC 6208
QY 1171 ATTGCCAACTGTAGATGACAACTGTAGATGTGACAGACCCCGGGTATCATATCGCAA 1230
Db 6209 TATGCCAACTGCAATCTTTGCTATGTAGTGTGCGGACCCCTCCCATGTTGTGCTCAA 6268
QY 1231 AATTATGGAGAGCTGTCTCTTAATAGATAGGCAATCATGCAATGCTCTATCCCTTAGAC 1290
Db 6269 GATGACAAACCAAGGCAATCAGCAATTAATTAAGAGGTGCTCTGAGATGATGCTTGAC 6328
QY 1291 GGAATAACTTTGAGGCTCAGTGGGAATTTGATGCAACTTATCAAAGAATATCTCAATA 1350
Db 6329 ACTTTTTCATTTAGGATCACATCTACATTTCAATGCTACATAGTGCAGACACTTCTCAATG 6388
QY 1351 CAAGATTCCTCAAGTAATCGTGACAGGCAATCTCGATATCTCGACTGAGCTTGGGAATGTC 1410
Db 6389 ATTAATGCAATTAATTTGTATCATCTAAGTCTCTAGACTTTGTCAAATCAAATCAATCAATA 6448
QY 1411 AACRACTCGATAAGTAAGTCTTTAGATAAGTTAGAGGAAAGCAAC 1455
Db 6449 AACAAATCTTTAAAGTCTGAGGATTTGATGAGATGCAATAGCAAC 6493

RESULT 12

US-10-670-695-35
; Sequence 35, Application US/10670695
; Publication No. US20040058316A1
; GENERAL INFORMATION:
; APPLICANT: Jensen, Wayne A.
; APPLICANT: Lappin, Michael R.
; APPLICANT: Rosen, David K.
; APPLICANT: Andrews, Janet S.
; TITLE OF INVENTION: USE OF RECOMBINANT ANTIGENS TO DETERMINE THE IMMUNE
; FILE REFERENCE: DI-9-1
; CURRENT APPLICATION NUMBER: US/10/670,695
; CURRENT FILING DATE: 2003-09-25
; PRIOR APPLICATION NUMBER: 09/521,738
; PRIOR FILING DATE: 2000-03-09
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 35
; LENGTH: 1986
; TYPE: DNA
; ORGANISM: canine distemper virus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(1986)
US-10-670-695-35

Query Match
Best Local Similarity 50.9%; Pred No. 3.2e-18; Length 1986;
Matches 220; Conservative 0; Mismatches 212; Indels 0; Gaps 0;
QY 330 AGGAGGAAACAGGAGCGCTTTATAGCGCCATTTATCGCGGTGCGAGCTCTCGGGTTGC 389
Db 654 AGGTAGGACAAAGCGCTTTGCGAGGAGTGTACTTGCAGGTGTAGCTTTAGGAGTGC 713
QY 390 ACCCGCTGACAGATAACAGAGCTTCGGCTCTGATACAGGCAACCAAAATGCTGCCAA 449

Db 714 TACAGCTGCACAAATCACTGCGAGGAATAGCTTTTACATCAATCCAACTCAATGCTCAAGC 773
QY 450 CATCTCGGCTTAAAGAGAGAAATGCTGCAACCAATGAGGCTGTGACAGGTCACATGA 509
Db 774 AATCCAATCTCTTAGAACACCGCTTGAAACAGTCTAAACAAAGCTATAGAAAGAAATTAGGGA 833
QY 510 TGGATTATCAAACTAGCAGTGGCAGTTGGGAAGATGCGACAAATTTGTTAATGACCAGTT 569
Db 834 GGCTACCAAGAAACCGCTATTGCCGTTTCAAGGAGTCAGGACTACGTCAACACGAAC 893
QY 570 TAAATAACAGCTCAGGAATGGACTGTATATAAATTAACAGGAGTTGGTGTAGAACT 629
Db 894 CGTCCCTGCCATGCAACATATGTCATGTGAATTTAGTTGGGAGAGATTTAGGCTTAAGACT 953
QY 630 CAACCTGTATCTAATGAAATGACTACAGTATTCGGGCCACAAATCACTTCCCTGCGCTT 689
Db 954 GCTTCGGTATTAATGAGTTGTTGTCATATTTGGCCGAGTTTACGTGACCCCTATTTC 1013
QY 690 AACCCAGCTGACTATCCAGGCGCTTTTACAATCTAGCTGGTGGGAATATGGAATTAATCTTT 749
Db 1014 AGCCGAGATATCAATTCAGGCACTGATTTATGCTCTTGGAGGAGAAATTCATAAGATACT 1073
QY 750 GACTAAGTTAGG 761
Db 1074 TGAGAAAGTTGGG 1085

RESULT 13

US-09-951-061A-86
; Sequence 86, Application US/09951061A
; Publication No. US20030082204A1
; GENERAL INFORMATION:
; APPLICANT: Paolletti, Enzo
; APPLICANT: Tartaglia, James
; APPLICANT: Taylor, Jill
; TITLE OF INVENTION: POXVIRUS - CANINE DISTEMPER VIRUS (CDV)
; TITLE OF INVENTION: RECOMBINANTS AND COMPOSITIONS AND METHODS EMPLOYING THE
; TITLE OF INVENTION: RECOMBINANTS
; NUMBER OF SEQUENCES: 143
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: McDonnell, Boehnen, Hulbert & Berghoff
; STREET: 300 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States of America
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/951,061A
; FILING DATE: 13-SEP-2001
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 09/354,138
; FILING DATE: 15-JUL-1999
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/224,657
; FILING DATE: 16-APR-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/073,962
; FILING DATE: 08-JUN-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/776,867
; FILING DATE: 23-OCT-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/621,614
; FILING DATE: 30-NOV-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/938,283
; FILING DATE: 31-AUG-1993

Best Local Similarity 50.9%; Pred. No. 5.4e-18;
Matches 220; Conservative 0; Mismatches 212; Indels 0; Gaps 0;

QY 330 AGGAGGGAACAGGAGCCCTTATAGCGCCATTATCGCGGTGCGAGTCTCGGGTTGC 389
Db 1422 AGGTAGGAGACAAAGCGCTTTTGCAGGAGTGTACTTGCAGGTGTAGCTTTAGGAGTGC 1363

QY 390 AACCGCTGCAGATACAGCAGCTTCGGCTCTGATACAGCCCAAAATGCTGCCAA 449
Db 1362 TACAGCTGCACAAATCATCTGAGGAATAGCTTTACATCAATCCAACTCAATGCTCAAGC 1303

QY 450 CATCTCCGGCTTAAAGAGAGAAATGCTGCAACCAATGAGGTGTGACGAGGTCACTGA 509
Db 1302 AATCCAAATCTTAGAACACCGCTTGAACAGCTTAAACAGCTATAGAGAAATTAGGA 1243

QY 510 TGGATTTACAACTAGCAGTGGCAGTGGGAGAGCAGCAATTTGTTAATGACCACTT 569
Db 1242 GGCTACCAAGAAACCGCTCATTTGCGGTTCCAGGAGTCCAGGACTACGTCAACACGA 1183

QY 570 TAATAAAACAGCTCAGGAATGGAGTGTATATAAAATTAACCCAGCAGGTGTGTAGA 629
Db 1182 CGTCCCTGCCATGCAATATGTCAATGTAATAGTTGGGAGAGATTAGGTTAGACT 1123

QY 630 CAACCTGTATCACTGAATGACTACAGTATTCGGGCCACAAATCACTTCCCTGCCCTT 689
Db 1122 GCTTCGGTATTATACAGTGTGTGTCAATATTTGGCCGAGTTTACGTGACCTTATTT 1063

QY 690 AACCCAGCTGACTATCCAGGCGCTTACAACTAGCTGTGGGATATGGAATTAAGTT 749
Db 1062 AGCCGAGATATCAATTCAGGCACTGATTATGCTCTTGGAGGAGAAATTCATAAGACT 1003

QY 750 GACTAAGTTAGG 761
Db 1002 TGGGAAGTTGG 991

RESULT 15
US-09-951-061A-93/c
Sequence 93, Application US/09951061A
Publication No. US20030082204A1
GENERAL INFORMATION:
APPLICANT: Paoletti, Enzo
APPLICANT: Tartaglia, James
APPLICANT: Taylor, Jill
APPLICANT: Gettig, Russell
TITLE OF INVENTION: POXVIRUS - CANINE DISTEMPER VIRUS (CDV)
TITLE OF INVENTION: RECOMBINANTS AND COMPOSITIONS AND METHODS EMPLOYING THE
TITLE OF INVENTION: RECOMBINANTS
NUMBER OF SEQUENCES: 143
CORRESPONDENCE ADDRESS:
ADDRESSEE: McDonnell, Boehnen, Hulbert & Berghoff
STREET: 300 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: United States of America
ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/951,061A
FILING DATE: 13-SEP-2001
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 09/354,138
FILING DATE: 15-JUL-1999
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/224,657
FILING DATE: 16-APR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/073,962
FILING DATE: 08-JUN-1993

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/776,867
FILING DATE: 23-OCT-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/621,614
FILING DATE: 30-NOV-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/938,283
FILING DATE: 31-AUG-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/621,614
FILING DATE: 30-NOV-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/105,483
FILING DATE: 12-AUG-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/847,951
FILING DATE: 06-MAR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/713,967
FILING DATE: 11-JUN-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07,666,056
FILING DATE: 07-MAR-1991
ATTORNEY/AGENT INFORMATION:
NAME: Frommer, William S.
REGISTRATION NUMBER: 25,506
REFERENCE/DOCKET NUMBER: 454310-2860
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 840-3333
TELEFAX: (212) 840-0712
INFORMATION FOR SEQ ID NO: 93:
SEQUENCE CHARACTERISTICS:
LENGTH: 4604 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
US-09-951-061A-93

Query Match 5.6%; Score 92.8; DB 10; Length 4604;
Best Local Similarity 50.9%; Pred. No. 5.6e-18;
Matches 220; Conservative 0; Mismatches 212; Indels 0; Gaps 0;

QY 330 AGGAGGGAACAGGAGCCCTTATAGCGCCATTATCGCGGTGCGAGTCTCGGGTTGC 389
Db 1530 AGGTAGGAGACAAAGCGCTTTTGCAGGAGTGTACTTGCAGGTGTAGCTTTAGGAGTGC 1471

QY 390 AACCGCTGCAGATACAGCAGCTTCGGCTCTGATACAGCCCAAAATGCTGCCAA 449
Db 1470 TACAGCTGCACAAATCACTGCGAGGAATAGCTTTACATCAATCCAACTCAATGCTCAAGC 1411

QY 450 CATCTCCGGCTTAAAGAGAGAAATGCTGCAACCAATAGGCTGTGACGAGGTCACTGA 509
Db 1410 AATCCAAATCTCTTAGAACCCGCTTGAACAGCTCTTAACAAAGCTATAGAAGAAATTAGGA 1351

QY 510 TGGATTTACAACTAGCAGTGGGAGATGCGACAAATTTGTTAATGACCACTT 569
Db 1350 GGCTACCCAGAAACCGCTCATTCGCTTACGGAGTCCAGGACTACGTCAACAGAACT 1291

QY 570 TAATAAAACAGCTCAGGAATGGAATGTATATAAAATTAACCCAGCAGGTGTGTAGAACT 629
Db 1290 CGTCCCTGCCATGCAACATATGTCAATGTAATAGTTAGTTGGGAGAGATTAGGTTAAAGACT 1231

QY 630 CAACCTGTATCACTGAATGACTACAGTATTCGGGCCCAAAATCACTTCCCTGCCCTT 689
Db 1230 GCTTCGGTATTATATCACTGAGTTGTGTCAATATTTGGCCCGAGTTTACGTGACCTTATTC 1171

QY 690 AACCCAGCTGACTATCCAGGCGCTTTTACAAATCTAGCTGGTGGGAATATGGAATTAAGTT 749
Db 1170 AGCCGAGATATCAATTCAGGCACTGATTATGCTCTTGGAGGAGAAATTCATAAGACT 1111

QY 750 GACTAAGTTAGG 761

Db 1110 TGGGAAGTTGGG 1099
|||||

Search completed: April 18, 2004, 01:19:10
Job time : 698 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: April 17, 2004, 06:54:07 ; Search time 3940 Seconds

(without alignments)
12596.686 Million cell updates/sec

Title: US-10-725-841-1

Perfect score: 1662

Sequence: 1 atgggctccagatcttctac.....gagccactacgaaatgtga 1662

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 27513289 seqs, 14931090276 residues

Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

EST:*

1: em_estba:*

2: em_esthum:*

3: em_estin:*

4: em_estmu:*

5: em_estov:*

6: em_estpl:*

7: em_estro:*

8: em_htc:*

9: gb_estl:*

10: gb_est2:*

11: gb_htc:*

12: gb_est3:*

13: gb_est4:*

14: gb_est5:*

15: em_estfun:*

16: em_estom:*

17: em_gss_hum:*

18: em_gss_inv:*

19: em_gss_pln:*

20: em_gss_vrt:*

21: em_gss_fun:*

22: em_gss_mam:*

23: em_gss_mus:*

24: em_gss_pro:*

25: em_gss_rod:*

26: em_gss_pbg:*

27: em_gss_vrl:*

28: gb_gss1:*

29: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	87.8	5.3	692	12	BG661033
2	43.2	2.6	801	29	BX213898
3	41	2.5	994	13	BX414650
4	40.8	2.5	816	28	BH183366

RESULT 1

BG661033

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

692 bp mRNA linear EST 26-APR-2001
N339 SSH-HCA-U library Homo sapiens cDNA, mRNA sequence.

BG661033

1 GI:13805211

EST.

Homo sapiens (human)

Homo sapiens

Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

Zhang, Z. and DuBois, R.N.

Detection of differentially expressed genes in human colon cancer

cells treatment with NS-398 using suppression subtractive

hybridization and differential screening

Unpublished (2000)

Contact: Zhonghua Zhang

Department of Medicine

Vanderbilt Medical Center

MCN C-2104, 1161 21st Ave. South, Nashville, TN 37212, USA

Tel: 615 343 1369

Fax: 615 343 6229

Email: zhonghua.zhang@mcmail.vanderbilt.edu

DNA sequencing by: Vanderbilt Medical Center

laboratory. This is a fragment of gene that up-regulated by NS-398

treatment.

C	5	40.8	2.5	816	29	CNS070JL	AL620307 T7 end of
C	6	39	2.3	387	12	BI072343	BI072343 C073F79U
C	7	39	2.3	463	29	CE051404	CE051404 tigr-gss-
C	8	39	2.3	474	13	BQ532151	BQ532151 APEX1_1_C
C	9	39	2.3	475	13	BQ529885	BQ529885 APEX1_3_H
C	10	39	2.3	480	13	BQ530741	BQ530741 APEX1_2_H
C	11	39	2.3	507	14	CD081007	CD081007 WA3-9999U
C	12	39	2.3	509	13	BQ532638	BQ532638 APEX2_7_G
C	13	39	2.3	517	13	BQ529996	BQ529996 APEX1_3_E
C	14	39	2.3	826	28	BH531701	BH531701 BOHGP20TF
C	15	38.8	2.3	406	10	AY032979	AY032979 AY032979
C	16	38.8	2.3	462	13	BQ531300	BQ531300 APEX1_2_C
C	17	38.8	2.3	463	13	BQ530551	BQ530551 APEX1_2_A
C	18	38.8	2.3	693	29	CC529583	CC529583 CH240_405
C	19	38.4	2.3	491	28	BZ267917	BZ267917 CH230_471
C	20	38.4	2.3	691	28	BH978172	BH978172 odel3a08
C	21	38.4	2.3	936	29	CNS00144	AL067742 Drosophila
C	22	38.2	2.3	311	10	BB237765	BB237765 BB237765
C	23	37.8	2.3	446	13	BQ529785	BQ529785 APEX1_3_F
C	24	37.6	2.3	885	13	BX425603	BX425603 BX425603
C	25	37.6	2.3	891	13	BU453464	BU453464 603771385
C	26	37.6	2.3	1099	28	CC273209	CC273209 CH261_37J
C	27	37.4	2.3	694	29	CE465529	CE465529 tigr-gss-
C	28	37.4	2.3	1200	13	BX387778	BX387778 BX387778
C	29	37.2	2.2	445	13	BQ530296	BQ530296 APEX1_3_B
C	30	37.2	2.2	446	13	BQ529830	BQ529830 APEX1_3_F
C	31	37.2	2.2	491	14	CD333801	CD333801 StrPU536
C	32	37.2	2.2	500	12	BP190449	BP190449 BP190449
C	33	37.2	2.2	1146	13	BX446722	BX446722 BX446722
C	34	37	2.2	268	9	AU227481	AU227481 AU227481
C	35	37	2.2	411	28	AZ556169	AZ556169 RPTC-23-1
C	36	37	2.2	522	28	AQ150073	AQ150073 HS-3194_A
C	37	36.8	2.2	860	29	CG332506	CG332506 OGMWC96TV
C	38	36.8	2.2	4254	11	AK083774	AK083774 Mus muscu
C	39	36.6	2.2	336	10	BB166428	BB166428 BB166428
C	40	36.6	2.2	571	29	CE103119	CE103119 tigr-gss-
C	41	36.4	2.2	787	29	CNS010B7	CNS010B7 Drosophila
C	42	36.4	2.2	1083	12	BM467292	BM467292 AGENCOURT
C	43	36.2	2.2	530	12	BJ360381	BJ360381 BJ360381
C	44	36.2	2.2	1022	29	CNS03RIF	AL257280 Tetraodon
C	45	36	2.2	312	12	BJ360628	BJ360628 BJ360628

ALIGNMENTS

Campus, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humbug@sanger.ac.uk Unpublished
This sequence was generated from the SP6 end of BAC 256K17. 256K17
is part of the Danokey BAC Library created by R. Plasterk and N.V.
keygene. Further details:
http://www.sanger.ac.uk/Projects/D_verio/.

FEATURES source

ORIGIN

	Query Match	2.6%	Score 43.2	DB 29	Length 801
	Best Local Similarity	54.4%	Pred. No. 0.26		
	Matches 87	Conservative 0	Mismatches 73	Indels 0	Gaps 0
Qy	1316	AATTTCGATCGA	CTTATCAAAAGAAATATCTCAATACAAGATCTCTCAAGTAATCGTGACAG	1375	
Db	228	AGATAAGGCAACTGGT	TATAATCTAAACAATAATGCAATTTTCATTTTAATTCGTATAGG	159	
Qy	1376	GCAATCTCGATATCTCGA	CTGAGCTTGGGAATGTCACAACTCGATAAGTAATGCTTTTAG	1435	
Db	168	ACGCTATTATATCTCTA	CTGATTTTGTTTGGTAAATATAGTACTATATAATGATATCT	109	
Qy	1436	ATAAGTTAGAGGAAACGA	CAACAGCAAACTAGACAAGGTCAA	1475	
Db	108	GTAAAATCTACTTTAAG	CGAGTGAAAAACAGTAAGGTTCAA	69	

RESULT	3
LOCUS	BX414650/c
DEFINITION	994 bp mRNA linear EST 15-MAY-2003 BX414650 Homo sapiens THYMUS cDNA clone CSOCAP001YN02
VERSION	3-PRIME, mRNA sequence.
KEYWORDS	BX414650 GI:30763455
SOURCE	EST.
ORGANISM	Homo sapiens (human) Homo sapiens Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE	1 (bases 1 to 994)
AUTHORS	Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
TITLE	Full-length cDNA libraries and normalization
JOURNAL	Unpublished (2001)
COMMENT	Contact : Genoscope

FEATURES source

ORIGIN

```
PCR Primers
FORWARD: 5'-CTAATACGACTCTACTATAGGC-3'
BACKWARD: 5'-TCGAGCGCGCCCGGCGAGGT-3'
Seq primer: M13 forward primer
High quality sequence stop: 692.
Location/Qualifiers
i. .692
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/db_xref="taxon:9606"
/cell_type="Colon cancer cell"
/cell_line="HCA-7"
/clone_lib="SSH:HCA-U library"
/note="Vector: pCR2.1-TOPO; Poly A RNA was isolated from
NS-398 treated and control cells, and suppression
subtractive hybridization was performed in forward and
reverse directions. The adapter sequences used in the
hybridization were as follows:
5'-CTAATACGACTCTACTATAGGCTCGAGCGCGCCCGGCGAGGT-3'
(adapter 1) and
5'-CTAATACGACTCTACTATAGGCAGCGTGGTCGCGGCCGAGGT-3' (adapter
2B)."

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Query Match	5.3%;	Score 87.8;	DB 12;	Length 692;
Best Local Similarity	51.5%;	Pred. No. 3.2e-15;		
Matches	201;	Conservative	0;	Mismatches 189; Indels 0; Gaps 0
344	QY	GAGCGCTTATAGGGCCGCAATATCGCGGTGACGCTCTCGGGTGTGCAACCGCTGCACAGA	403	
297	Db	GCGGATTTGCAGGGGTGGTGAATTGATTAGCTGCAATTAGGAGTAGCTACTGCGGCACAGG	356	
404	QY	TAAACAGCAGCTTCGGCTCTGTATCAACAGCAACCAAAATGCTGCCAACATCTCTCCGGCTTA	463	
357	Db	TCCTGCGCGCAGTAGCACTAGTAAAGGCAATGAAATGCTGCGGCTACTCTCAATCTCA	416	
464	QY	AAGAGAGAAATTGTCGCAACCAATGAGGCTGTGCAGGCTCACTGATGGATTATCACAAAC	523	
417	Db	AAAATGCAATCCAAAAACAATCGGCAGTTGACAGCGTGGTCCAGGCCACACAATCAC	476	
524	QY	TAGCAGTGGCAGTTGGGAAGATGACGCAATTTGTTAATGACGAGTTAATAAAACAGCTC	583	
477	Db	TAGGAACGGCAGTTCAAGCAGTTCAAGATCATATAAACAGTGTGTTAGTCCAGCAATTA	536	
584	QY	AGGAATTGGACTGTATATAAAATTACCCAGCAGGTTGGTGTAGAACTCAACCTGTATCTAA	643	
537	Db	CAGCAGCCAACTGTAAAGSCCAAGATGCTATCATTTGGCTCAATCCTCAATCTCTATTGGA	596	
644	QY	CTGAATTGACTTACAGTATTTGGGCCACAAAATCACTTCCCTTGCCCTTAACCCAGCTGCATTA	703	
597	Db	CCGAGTTGACAACTATCTTCCACAAATCAAAATACAAACCCCTGCATTGAGTCTTATTACAA	656	
704	QY	TCCAGGCGCTTTTACAATCTAGCTGGTGGGA	733	
657	Db	TTCAAGCTTTAAGGATTCTACTGGGGAGTA	686	

RESULT 2					
EX213898/c					
LOCUS	EX213898	801 bp	DNA	linear	GSS 29-JAN-2003
DEFINITION	Danio rerio genomic clone DKEY-256K17, genomic survey sequence.				

REFERENCE
AUTHORS
TITLE
JOURNAL

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Query Match          2.5%; Score 41; DB 13; Length 994;
Best Local Similarity 19.7%; Pred. No. 1.4;
Matches 92; Conservative 167; Mismatches 206; Indels 3; Gaps 1;

QY 1177 AACTGTAAGTGCACACATGTAGATGTGCGACACCCCGGATCATCATATCGCAAAATAT 1236
    ||| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 946 AAARWRDRWTAAWAARKKWADWTITKTKKADADWDGDDWDATAWWAADDDAW 887

QY 1237 GGAGAAGCTGTCTCTTAATAGATAGGCAATCATGCAATGTCCTATCTTAGACGGAATA 1296
    ||| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 986 AARWAAATWTTDMDT--AWTRKDKATWKADDDAKTKTTTTTTTTTKWKAATDAGWT 830

QY 1297 ACTTTGAGGCTCAGTGGGGAATTTGATGCACTTATCAAGAATATCTCAATACAGAT 1356
    ||| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 829 AKWADATWADAADAAARAAWRAAAWAAADADWWWWDAADAAWAAWD 770

QY 1357 TCTCAAGTATCTGTCAGGCAATCTCGATATCTCGACTGAGCTTGGGAATGTCAACAAC 1416
    ||| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 769 TKDKRAWAADWAFAAAAAAWDWRGRADAAKDKARAANWDGAGRDKDRDWAARWD 710

QY 1417 TCGTAAGTATGCTTTAGATAAGTTAGAGAAAGCAACAGCAAACTAGACAAAGTCAAT 1476
    ||| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 709 DADAARRAAAAAATATWATWTKWKDKDWAATAAATATKKGKRDARDWAAATTTT 650

QY 1477 GTCAAACTGACCAACATCGCTCTCATCACCTATATCTGTTTAACTGTCATATCTTT 1536
    ||| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 649 TTTTAAWADKAWKKWATTTTTTTTTTTTTTTTTTKTKTTAKWTWDADWTTTTTT 590

QY 1537 GTTTGGTATCTACTTACGCTGGTTCTAGCATGCTACCTGATGTAACAAGCAAAAGCGCAA 1596
    ||| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 589 TTTTWTWAAATTKTKTKTKTKTKTKTKTKTKTKTKTKTKTKTKTKTKTKTKTKTKTKTK 530

QY 1597 CAGAAGCTTTGATGCTTGGGAATTAACCTGATGATGATGATGATGATGATGATGATG 1644
    ||| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 529 RRGRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 482
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RESULT 4
BH183366/c
LOCUS          816 bp      DNA      linear      GSS 19-OCT-2001
DEFINITION    023_G.14-21 SmBAC1 Schistosoma mansoni genomic clone 023G14 5',
              genomic survey sequence.
ACCESSION     BH183366
VERSION       BH183366.1 GI:16288520
KEYWORDS      GSS:
SOURCE        Schistosoma mansoni
ORGANISM      Schistosoma mansoni
REFERENCE     1 (bases 1 to 816)
AUTHORS      Eukaryota; Metazoa; Platyhelminthes; Trematoda; Digenea;
              Strigeidida; Schistosomatoidea; Schistosomatidae; Schistosoma.
TITLE        Le Paslier,M.C., Pierce,R.J., Merlin,F., Hirai,H., Wu,W.,
              Williams,D.L., Johnston,D., LoVerde,P.T. and Le Paslier,D.
              Construction and characterization of a Schistosoma mansoni
              bacterial artificial chromosome library
              Genomics 65 (2), 87-94 (2000)
JOURNAL       20247247
MEDLINE       10783255
PUBMED       Other_GSSs: 023_G.14-rev
              Contact: Pierce RJ
              INSERM U 167
              Institut Pasteur de Lille
              1 rue du Professeur A. Calmette, 59019-Lille, France
              Tel: (33) (0)3 20877783
              Fax: (33) (0)3 20877888
              Email: Raymond.Pierce@pasteur-lille.fr
              CNS sequencing ID=DG0AA023BD07Cp1
              Plate: 023 row: G column: 14
              Seq primer: M13 -21 primer
              Class: BAC ends
              High quality sequence stop: 816.
              Location/Qualifiers
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/mol_type="genomic DNA"
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/db_xref="taxon:6183"
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/sex="mixed"
/dev_stage="cercariae"
/lab_host="Biomphalaria glabrata"
/clone_lib="SmBAC1"
/notes="Vector: pBeloBAC 11; Site 1: Hind III; Partially
Hind III digested and size-selected S. mansoni cercarial
DNA was ligated into Hind III digested pBeloBAC 11 vector
and used to transform E. coli DH10B. The complete library
contains 23808 clones from 4 independent
sizing-ligation-transformations. Average insert size
ranges from 70-127 kb and genome coverage is 7.9-fold."

ORIGIN

Query Match          2.5%; Score 40.8; DB 28; Length 816;
Best Local Similarity 35.4%; Pred. No. 1.4;
Matches 80; Conservative 41; Mismatches 105; Indels 0; Gaps 0;

QY 1329 TTATCAAAAGATATCTCAATACAAAGATTTCTCAAGTAATCTGTCAGCGCAATCTCGATAT 1388
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 536 TTAGAGAAAAAATATATATATATATATAAATAAATAAATAAATAAATAAATAAATAAATAA 477

QY 1389 CTGAGTACGCTGGGAATGTCACAACTCGAATGTAAGTAAGTTCCTTAGATAGTTCAGGGA 1448
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 476 ATATATATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 417

QY 1449 AAGCAACAGCAAACTAGCAAGCTCAATGTCACAACTGACAGCAGCATCCGCTCTCATCAC 1508
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 416 AAAAAAAYAAAGATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATA 357

QY 1509 CTATATCGTTTAACTGTCATATCTCTTGTGTTGGTATATCTTAGC 1554
    ||| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 356 YGYBYKYTKYTGTTGKTGKTGKTGKTGKTGKTGKTGKTGKTGKTGKTGKTGKTGKTGKTG 311

RESULT 5
CNS070JL/c
LOCUS          816 bp      DNA      linear      GSS 30-NOV-2001
DEFINITION    T7 end of clone 023BD07 of library SmBAC1 from strain Puerto-Rican
              of Schistosoma mansoni, genomic survey sequence.
ACCESSION     AL620307
VERSION       AL620307.1 GI:16034449
KEYWORDS      GSS:
SOURCE        Schistosoma mansoni
ORGANISM      Schistosoma mansoni
REFERENCE     1 (bases 1 to 816)
AUTHORS      Eukaryota; Metazoa; Platyhelminthes; Trematoda; Digenea;
              Strigeidida; Schistosomatoidea; Schistosomatidae; Schistosoma.
TITLE        Le Paslier,M.C., Pierce,R.J., Merlin,F., Hirai,H., Wu,W.,
              Williams,D.L., Johnston,D., LoVerde,P.T. and Le Paslier,D.
              Construction and characterization of a Schistosoma mansoni
              bacterial artificial chromosome library
              Genomics 65 (2), 87-94 (2000)
JOURNAL       20247247
MEDLINE       10783255
PUBMED       Other_GSSs: 023_G.14-rev
              Contact: Pierce RJ
              INSERM U 167
              Institut Pasteur de Lille
              1 rue du Professeur A. Calmette, 59019-Lille, France
              Tel: (33) (0)3 20877783
              Fax: (33) (0)3 20877888
              Email: Raymond.Pierce@pasteur-lille.fr
              CNS sequencing ID=DG0AA023BD07Cp1
              Plate: 023 row: G column: 14
              Seq primer: M13 -21 primer
              Class: BAC ends
              High quality sequence stop: 816.
              Location/Qualifiers
              1. .816
              /organism="Schistosoma mansoni"
              /mol_type="genomic DNA"
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/strain="Puerto-Rican"
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ORIGIN

Query Match 2.5%; Score 40.8; DB 29; Length 816;
Best Local Similarity 35.4%; Pred. No. 1.4; Mismatches 0; Gaps 0;
Matches 80; Conservative 41; Indels 105; Indels 0; Gaps 0;
QY 1329 TTATCAAGAATATCTCAATCAAGATTCTCAAGTAATCTGACAGGCAATCTCGATAT 1388
DB 536 TTAGAGAAAANATATATATATAATATAATATAATATAATATAATATAATATAATAT 477
QY 1389 CTCGACTGAGCTGGGAATGTCACAACTCGATAGTAAGTAATGCTTTAGATAAGTAGAGA 1448
DB 476 ATATATATAANAATAAATAATATAATAATTTATATAAATAAATAAATAAATAAATAA 417
QY 1449 AAGCAACAGCAACATAGACAGGTCATGTCATCAATGTCATCAACCTGACGACATCGCTCTCATCAC 1508
DB 416 AAAAAAAYAAAGATATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 357
QY 1509 CTATATCGCTTTAACTGTCATATCTCTTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG 1554
DB 356 YGYBYKYKYTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 311

RESULT 6

BI072343/c
LOCUS BI072343 387 bp mRNA linear EST 19-JUN-2001
DEFINITION C073P790 Populus strain T89 leaves Populus tremula x Populus tremuloides cDNA, mRNA sequence.
ACCESSION BI072343
VERSION BI072343.1 GI:14492963
KEYWORDS EST.
SOURCE Populus tremula x Populus tremuloides
ORGANISM Populus tremula x Populus tremuloides
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids I; Malpighiales; Salicaceae; Populus.
REFERENCE 1 (bases 1 to 387)
Jansson,S., Bhalarao,R., Erlandsson,R., Bjorkbacka,H., Karlsson,J., Sterky,F., Gustafsson,P. and Lundberg,J.
AUTHORS Gene expression in Populus leaves
TITLE Unpublished (2001)
JOURNAL Contact: Erlandsson R
COMMENT Department of Biotechnology
Royal Institute of Technology
Teknikringen 30, Stockholm S-10044, Sweden
Tel: 46 8 790 8287
Fax: 46 8 245452
Email: rikeri@biochem.kth.se.

FEATURES

source
1..387
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/mol_type="mRNA"
/strain="T89"
/db_xref="taxon:47664"
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Matches 129; Conservative 0; Indels 151; Indels 0; Gaps 0;
QY 1309 AGTGGGAATTTGATCGCACTTATCAAAAGATATCTCAATCAAGATTTCTCAAGTAATC 1368
DB 303 AGTGATGAACCTTTTCCATCTCTCACTACAAATTTCTCTCCACAACTTTTGACATAAA 244
QY 1369 GTGACAGGAATCTCGATATCTCGATGAGCTGGGAATGTCACAACTCGGATAGTAAT 1428

DB 243 CTTGAAGGCATTGTGGCAATCACACAGATCCTAAGATTTCTTAAAAACCCCTGACCGTAGC 184
QY 1429 GCTTTAGATAGTTAGAGGAAGCAACAGCAAACTAGACAAAGTCAATGTCAAACTGACC 1488
DB 183 TCCATGGGGAAGTTTCATAAATCCATAAGCAACTGCGAGCTTCTCCTACTATGATGACAA 124
QY 1489 AGCACATCCGCTCTCATCACCTATATCGTTTAACTGTCATATCTCTTGTGTTGTTGTTG 1548
DB 123 CTCATGTTCTTTAGATCAGATTCACATCAATGCAACACATCTTTGTTGTCAGGCACATA 64
QY 1549 CTTAGCCCTGTTCTAGCATGCTACTGATGTACAGCAAA 1588
DB 63 CCCTATCTTCTCTATTTCCAAAGACCAGTTGCTCANGGTAA 24
RESULT 7
CE051404 463 bp DNA linear GSS 24-SEP-2003
LOCUS tigr-gss-dog-17000358155421 dog Library Canis familiaris genomic,
DEFINITION genomic survey sequence.
ACCESSION CE051404
VERSION CE051404.1 GI:35094024
KEYWORDS GSS.
SOURCE Canis familiaris (dog)
ORGANISM Canis familiaris
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
REFERENCE 1 (bases 1 to 463)
Kirkness,E.F., Hafna,V., Halpern,A.L., Levy,S., Remington,K.,
Rusch,D.B., Delcher,A.L., Pop.M., Wang,W., Fraser,C.M. and
Venter,J.C.
TITLE The dog genome: survey sequencing and comparative analysis
JOURNAL Science 301 (5641), 1898-1903 (2003)
MEDLINE 22875432
PUBMED 14512627
COMMENT Contact: Kirkness EF
The Institute for Genomic Research
Department of Eukaryotic Genomics, TIGR, 9712 Medical Center Drive,
Rockville, MD 20850, USA
Tel: 301-838-0200
Fax: 301-838-0208
Email: ekirknes@tigr.org
Class: shotgun.
FEATURES
source
1..463
/organism="Canis familiaris"
/mol_type="genomic DNA"
/strain="Standard Poodle"
/db_xref="taxon:9615"
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/note="Site 1: BstXI; Libraries were prepared from
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Best Local Similarity 48.8%; Pred. No. 3.7;
Matches 105; Conservative 0; Mismatches 110; Indels 0; Gaps 0;
QY 565 CAGTTTATAAACAAGCTCAGCAATGGACTGTATAAATAATACCAGAGTTGTTGTTA 624
DB 327 CAATAAAGAAAAAAGCTCACTTTTGACACTGTAACTAGGTCAACAGTGCAGGACAA 268
QY 625 GAACCTCAACCTGTATCTAATGAACTGAGTATCGGSCCAACAATCACTTCCCT 684
DB 267 GAATTCATATTGAACCTGAAGTTTTCATATACATTAATTAACAATATTATACCTCT 208
QY 685 GCCTTAAACCAAGCTGACTATCCAGCGCTTTACAACTAGCTGTGGGGAATAGGATAC 744
DB 207 TTCTTAACATAAATCAACATGCAGCTCAATTTAGATATAAATTTGGTACATTATATAT 148
QY 745 TTGTTGACTAGTTAGGTGTAGGACCAACCACT 779
DB 147 ATATATATATATATATATTGTTGTTTCTCAATATT 113

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RESULT 8
BQ532151
LOCUS
DEFINITION APEX1.1 C10 pSLR Saccharum officinarum cDNA 5', mRNA linear EST 06-AUG-2003
ACCESSION BQ532151
VERSION BQ532151.1 GI:33459914
KEYWORDS EST.
SOURCE Saccharum officinarum
ORGANISM Saccharum officinarum
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
            clade; Panicoideae; Andropogoneae; Saccharum.
REFERENCE
AUTHORS Schulze,S.R., Ma,H.M., Meizhu Yang,J., Bowers,J.E., Mirkov,E. and
            Paterson,A.H.
            An EST survey of the sugarcane transcriptome
            Unpublished (2002)
            Contact: Paterson, A.H.
            Plant Genome Mapping Laboratory
            University of Georgia, Center for Applied Genetic Technologies
            111 Riverbend Rd., Athens, GA 30602, USA
            Tel: 706 583 0162
            Fax: 706 583 0160
            Email: paterson@dogwood.botany.uga.edu
            Plate: 1 row: C column: 10
            Seq primer: M13 Rev.
FEATURES
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            /mol_type="mRNA"
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            /tissue_type="Leafroll including apex"
            /dev_stage="After floral induction"
            /clone_lib="pSLR"
            /notes="Vector: UniZAP XR/pBluescript; Site_1: EcoRI;
            Site_2: XhoI"
ORIGIN
Query Match 2.3%; Score 39; DB 13; Length 474;
Best Local Similarity 50.8%; Pred. No. 3-7;
Matches 93; Conservative 0; Mismatches 90; Indels 0; Gaps 0;
QY 370 GGTGCAGCTCTCGGGTTGCACCGCTGCACAGATACACAGCTTGGCTCTGTATACAA 429
    |||||
Db 283 GGTGACGCGTTGGCGTGGATGGCGGCGAGAGGAGCAACAGTTCGCCCTCTGGTTTGA 342
QY 430 GCCAACCAAAATGCTGCCACATCTCCGGCTTAAGAGAGAGATTGCTGCAACCAATGAG 489
    |||||
Db 343 CCCACCAAGACTTCCATACCTACTCCATCTCTGGAATCCCAAGACGTCATCTTCAT 402
QY 490 GCTGTGCACGAGTCACTGATGATTATCAAACTAGCAGTGGCAGTTGGGAAGATGCAG 549
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Db 403 GGTGGACGAGATCCCATACCTACTCCATCTCTGGAATCCCAAGACGTCATCTTCAT 402
QY 550 CAA 552
    |||
Db 463 CAA 465

RESULT 9
BQ529885
LOCUS
DEFINITION APEX1.3 E11 pSLR Saccharum officinarum cDNA 5', mRNA linear EST 06-AUG-2003
ACCESSION BQ529885
VERSION BQ529885.1 GI:33457648
KEYWORDS EST.
SOURCE Saccharum officinarum
ORGANISM Saccharum officinarum
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
            clade; Panicoideae; Andropogoneae; Saccharum.
REFERENCE
AUTHORS Schulze,S.R., Ma,H.M., Meizhu Yang,J., Bowers,J.E., Mirkov,E. and
            Paterson,A.H.
            An EST survey of the sugarcane transcriptome
            Unpublished (2002)
            Contact: Paterson, A.H.
            Plant Genome Mapping Laboratory
            University of Georgia, Center for Applied Genetic Technologies
            111 Riverbend Rd., Athens, GA 30602, USA
            Tel: 706 583 0162
            Fax: 706 583 0160
            Email: paterson@dogwood.botany.uga.edu
            Plate: 1 row: C column: 10
            Seq primer: M13 Rev.
FEATURES
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            1..474
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            /clone_lib="pSLR"
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            Site_2: XhoI"
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QY 490 GCTGTGCACGAGTCACTGATGATTATCAAACTAGCAGTGGCAGTTGGGAAGATGCAG 549
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Db 403 GGTGGACGAGATCCCATACCTACTCCATCTCTGGAATCCCAAGACGTCATCTTCAT 402
QY 550 CAA 552
    |||
Db 463 CAA 465

RESULT 10
BQ530741
LOCUS
DEFINITION APEX1.2 H11 pSLR Saccharum officinarum cDNA 5', mRNA linear EST 06-AUG-2003
ACCESSION BQ530741
VERSION BQ530741.1 GI:33458504
KEYWORDS EST.
SOURCE Saccharum officinarum
ORGANISM Saccharum officinarum
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
            clade; Panicoideae; Andropogoneae; Saccharum.
REFERENCE
AUTHORS Schulze,S.R., Ma,H.M., Meizhu Yang,J., Bowers,J.E., Mirkov,E. and
            Paterson,A.H.
            An EST survey of the sugarcane transcriptome
            Unpublished (2002)
            Contact: Paterson, A.H.
            Plant Genome Mapping Laboratory
            University of Georgia, Center for Applied Genetic Technologies
            111 Riverbend Rd., Athens, GA 30602, USA
            Tel: 706 583 0162
            Fax: 706 583 0160
            Email: paterson@dogwood.botany.uga.edu
            Plate: 1 row: E column: 11
            Seq primer: M13 Rev.
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            Site_2: XhoI"
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Best Local Similarity 50.8%; Pred. No. 3-7;
Matches 93; Conservative 0; Mismatches 90; Indels 0; Gaps 0;
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QY 430 GCCAACCAAAATGCTGCCACATCTCCGGCTTAAGAGAGAGATTGCTGCAACCAATGAG 489
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QY 490 GCTGTGCACGAGTCACTGATGATTATCAAACTAGCAGTGGCAGTTGGGAAGATGCAG 549
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Db 403 GGTGGACGAGATCCCATACCTACTCCATCTCTGGAATCCCAAGACGTCATCTTCAT 402
QY 550 CAA 552
    |||
Db 463 CAA 465

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clade; Panicoideae; Andropogoneae; Saccharum.

1 (bases 1 to 475)
Schulze,S.R., Ma,H.M., Meizhu Yang,J., Bowers,J.E., Mirkov,E. and
Paterson,A.H.

An EST survey of the sugarcane transcriptome

Unpublished (2002)

Contact: Paterson, A.H.

Plant Genome Mapping Laboratory

University of Georgia, Center for Applied Genetic Technologies

111 Riverbend Rd., Athens, GA 30602, USA

Tel: 706 583 0162

Fax: 706 583 0160

Email: paterson@dogwood.botany.uga.edu

Plate: 3 row: E column: 11

Seq primer: M13 Rev.

Location/Qualifiers

source

1..475

/organism="Saccharum officinarum"

/mol_type="mRNA"

/cultivar="CP72-2086"

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/tissue_type="Leafroll including apex"

/dev_stage="After floral induction"

/clone_lib="pSLR"

/note="Vector: UniZAP XR/pBluescript; Site_1: EcoRI;

Site_2: XhoI"

ORIGIN

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Best Local Similarity 50.8%; Pred. No. 3-7;

Matches 93; Conservative 0; Mismatches 90; Indels 0; Gaps 0;

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QY 430 GCCAACCAAAATGCTGCCACATCTCCGGCTTAAGAGAGAGATTGCTGCAACCAATGAG 489

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Db 343 CCCACCAAGACTTCCATACCTACTCCATCTCTGGAATCCCAAGACGTCATCTTCAT 402

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QY 550 CAA 552

|||

Db 463 CAA 465

RESULT 10

BQ530741

LOCUS

DEFINITION APEX1.2 H11 pSLR Saccharum officinarum cDNA 5', mRNA linear EST 06-AUG-2003

ACCESSION BQ530741

VERSION BQ530741.1 GI:33458504

KEYWORDS EST.

SOURCE Saccharum officinarum

ORGANISM Saccharum officinarum

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD

clade; Panicoideae; Andropogoneae; Saccharum.

1 (bases 1 to 480)

Schulze,S.R., Ma,H.M., Meizhu Yang,J., Bowers,J.E., Mirkov,E. and

Paterson,A.H.

An EST survey of the sugarcane transcriptome

Unpublished (2002)

Contact: Paterson, A.H.

Plant Genome Mapping Laboratory

University of Georgia, Center for Applied Genetic Technologies

111 Riverbend Rd., Athens, GA 30602, USA

Tel: 706 583 0162

Fax: 706 583 0160

Email: paterson@dogwood.botany.uga.edu

RESULT 9

BQ529885

LOCUS

DEFINITION APEX1.3 E11 pSLR Saccharum officinarum cDNA 5', mRNA linear EST 06-AUG-2003

ACCESSION BQ529885

VERSION BQ529885.1 GI:33457648

KEYWORDS EST.

SOURCE Saccharum officinarum

ORGANISM Saccharum officinarum

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD

Plate: 2 row: H column: 11
Seq primer: M13 Rev.

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ORIGIN

Query Match 2.3%; Score 39; DB 13; Length 480;

Best Local Similarity 50.8%; Pred. No. 3.8;
Matches 93; Conservative 0; Mismatches 90; Indels 0; Gaps 0;

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QY 430 GCCAACCAAAATGTCGCAACATCTCTCGGCTTAAGAGAGAATTCGTCGAACCAATGAG 489
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Db 343 CCCACCAAGGACTTCCATCTACTCTCTGGAATCCCAAGCAGCTCATCTTCAT 402
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QY 490 GCTGTGACGAGGTCACGTGATGATATCAACATAGCAGTGGCGATGGGAAGATGAG 549
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QY 550 CAA 552
|||||
Db 463 CAA 465

RESULT 11

CD081007
LOCUS 507 bp mRNA linear EST 14-SEP-2003
DEFINITION MA3-9999U-M317-D07-U.G MA3-0001 Schistosoma mansoni cDNA clone
ACCESSION MA3-9999U-M317-D07.6, mRNA sequence.
VERSION CD081007.1 GI:34632000
KEYWORDS EST.
SOURCE Schistosoma mansoni
ORGANISM Schistosoma mansoni
Eukaryota; Metazoa; Platyhelminthes; Trematoda; Digenea;
Strigoidida; Schistosomatoidea; Schistosomatidae; Schistosoma.
1 (bases 1 to 507)
Verjovsky-Almeida, S., DeMarco, R., Martins, E.A.L., Guimaraes, P.E.M.,
Ojopi, E.P.B., Paquola, A.C.M., Piazza, J.P., Nishiyama, M.Y. Jr.,
Kitajima, J.P., Adamson, R.E., Ashton, P.D., Bonaldo, M.F., Jr.,
Coulson, P.S., Dillon, G.P., Farias, L.P., Gregorio, S.P., Ho, P.L.,
Leste, R.A., Malaquias, L.C.C., Marques, R.C.P., Miyasato, P.A.,
Nascimento, A.L.T.O., Ohlweiler, F.P., Reis, E.M., Ribeiro, M.A.,
Sa, R.G., Stukart, G.C., Soares, M.B., Gargioni, C., Kawano, T.,
Rodrigues, V., Madeira, A.M.B.N., Wilson, R.A., Menck, C.F.M.,
Setubal, J.C., Leite, L.C.C. and Dias-Neto, E.

Transcriptome analysis of the acoelomate human parasite Schistosoma
mansoni

Nat. Genet. 35 (2), 148-157 (2003)

22879926

Contact: Dr. Sergio Verjovsky-Almeida

Departamento de Bioquímica

Instituto de Química - Universidade de São Paulo

Av. Prof. Lineu Prestes 748 sala 1200, 05508-900 São Paulo - SP,

Brasil

Tel: +55-11-3091-2173

Fax: +55-11-3091-2186

Email: verjoi@iq.usp.br

This sequence was derived from the FAPESP Schistosoma mansoni EST
Genome Project. All sequences in the project were assembled and
annotated. This entry and all the assembled sequences can be seen

in the following URL <http://bioinfo.iq.usp.br/schisto/>
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ORIGIN

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Matches 87; Conservative 0; Mismatches 94; Indels 0; Gaps 0;

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QY 1492 ACATCCGCTCATCACCTATATCTTTAACTGTCTATCTCTTTGTGGTATACTT 1551
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Db 187 TAAACCTGTCTCATCAGCTTTATTCCTTGAATAATTATTTCAGACATTTAATCGTCACTT 246
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QY 1552 AGCTGTGTTTACGATGCTACTGATGTAAGCAAAAGGCGCAAGAACCTTGTTA 1611
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Db 247 GGATCCAATCTTCATGTTACGTTTACCAAGCGATNNNNNNNNNNNAGCAATAA 306
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QY 1612 T 1612
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Db 307 T 307

RESULT 12

BQ532638
LOCUS 509 bp mRNA linear EST 06-AUG-2003
DEFINITION APEX2.7 G05 PSLR Saccharum officinarum cDNA 5', mRNA sequence.
ACCESSION BQ532638
VERSION BQ532638.1 GI:33460401
KEYWORDS EST.
SOURCE Saccharum officinarum
ORGANISM Saccharum officinarum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Saccharum.
1 (bases 1 to 509)
Schulze, S.R., Ma, H.M., Meizhu Yang, J., Bowers, J.E., Mirkov, E. and
Paterson, A.H.

REFERENCE

AH

AUTHORS

Paterson, A.H.

An EST survey of the sugarcane transcriptome

Unpublished (2002)

TITLE

Plant Genome Mapping Laboratory

University of Georgia, Center for Applied Genetic Technologies

111 Riverbend Rd., Athens, GA 30602, USA

Tel: 706 583 0162

Fax: 706 583 0160

Email: paterson@dogwood.botany.uga.edu

Plate: 7 row: G column: 05

Seq primer: M13 Rev.

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Site_2: XhoI"

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QY 430 GCCAACCAAAATGCTGCCAATCTCTCGGCTTAAAGAGAGAATGTGCAACCAATGAG 489
D 343 CCCACCAAGGACTTCATACCTACTCTCTGGAATCCCAAGCAGCTCATCTTCAT 402
QY 490 GCTGTGACGAGGTCAGTGTGATTATCAACACTAGCAGTGGCAGTTGGAGATCGAG 549
D 403 GTGGAGCAGATGCCCATCAGGACTTCCGGAACCTGGAGAGCAAGGGGTGGGTTCCC 462
QY 550 CAA 552
D 463 CAA 465

RESULT 14
BH531701
LOCUS BH531701
DEFINITION BOHGP20TF BOHG Brassica oleracea genomic clone BOHGP20, genomic
survey sequence.
ACCESSION BH531701
VERSION BH531701.1 GI:17752135
KEYWORDS GSS.
SOURCE Brassica oleracea
ORGANISM Brassica oleracea
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
REFERENCE 1 (bases 1 to 826)
AUTHORS Town,C.D., Van Aken,S., Utterback,T., Koo,H. and Fraser,C.M.
TITLE Whole genome shotgun sequencing of Brassica oleracea
JOURNAL Unpublished (2001)
COMMENT Other GSSs: BOHGP20TR
Contact: Chris Town
TIGR
9712 Medical Center Drive, Rockville, MD 20850, USA.
Tel: 301-838-3523
Fax: 301-838-0208
Email: cdtown@tigr.org
DNA is from a doubled haploid provided by Tom Osborn.
Seq primer: TF
Class: sheared ends.

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genomic DNA inserted into pHOS1 using BstXI linkers"

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QY 629 TCAACCTGTATCTAACTGAATTCAGTACAGTATTCGGGCCACAAATCATCTTCCCTGCCT 688
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D 343 CCCACCAAGGACTTCATACCTACTCTCTGGAATCCCAAGCAGCTCATCTTCAT 402
QY 490 GCTGTGACGAGGTCAGTGTGATTATCAACACTAGCAGTGGCAGTTGGAGATCGAG 549
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QY 550 CAA 552
D 463 CAA 465

RESULT 13
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DEFINITION APEX1 3 E01 pSLR Saccharum officinarum cDNA 5', mRNA sequence.
ACCESSION BQ529996
VERSION BQ529996.1 GI:33457759
KEYWORDS EST.
SOURCE Saccharum officinarum
ORGANISM Saccharum officinarum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACAD
clade; Panicoideae; Andropogoneae; Saccharum.
REFERENCE 1 (bases 1 to 517)
AUTHORS Schulze,S.R., Ma,H.M., Meizhu Yang,J., Bowers,J.E., Mirkov,E. and
Paterson,A.H.
TITLE An EST survey of the sugarcane transcriptome
JOURNAL Unpublished (2002)
COMMENT Contact: Paterson, A.H.
Plant Genome Mapping Laboratory
University of Georgia, Center for Applied Genetic Technologies
111 Riverbend Rd., Athens, GA 30602, USA
Tel: 706 583 0162
Fax: 706 583 0160
Email: paterson@dogwood.botany.uga.edu
Plate: 3 row: E column: 01
Seq primer: M13 Rev.

FEATURES
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Site 2: XhoI"

ORIGIN
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QY 430 GCCAACCAAAATGCTGCCAATCTCTCGGCTTAAAGAGAGAATGTGCAACCAATGAG 489
D 343 CCCACCAAGGACTTCATACCTACTCTCTGGAATCCCAAGCAGCTCATCTTCAT 402

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: April 17, 2004, 06:54:07 ; Search time 97 Seconds
(without alignments)
1610.812 Million cell updates/sec

Title: US-10-725-841-2

Perfect score: 2757

Sequence: 1 MGRSSTRIPVPLMLTVRVA.....KTLWLGNNTLDQWRATTKM 553

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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1: Geneseqp1990s.*

2: Geneseqp1990s.*

3: Geneseqp2000s.*

4: Geneseqp2001s.*

5: Geneseqp2002s.*

6: Geneseqp2003as.*

7: Geneseqp2003bs.*

8: Geneseqp2004s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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3	2620	95.0	1103	6	ABR39678
4	2616	94.9	553	3	AAV51231
5	2610	94.7	553	2	AAR58858
6	2610	94.7	553	2	AAR49141
7	2610	94.7	553	2	AAW06828
8	2610	94.7	553	2	AAW10691
9	2610	94.7	553	3	AAV58183
10	2610	94.7	553	3	AAV21983
11	2610	94.7	553	3	AAV58183
12	2606	94.5	553	2	AAV21983
13	2606	94.5	553	2	AAV21983
14	2603	94.4	553	1	AAV70176
15	2493.5	90.4	564	5	ABG31709
16	2401	87.1	526	1	AAP80986
17	2386	86.5	526	2	AAR20501
18	2086.5	75.7	436	6	ABO10250
19	2085	74.9	437	4	AAU14030
20	717	26.0	529	6	ABJ18515
21	715	25.9	529	6	ABJ18516
22	714	25.9	551	6	ABJ18506
23	712	25.8	551	6	ABJ18514
24	707	25.6	551	6	ABJ18513
25	706	25.6	529	4	ABP98712

ALIGNMENTS

RESULT 1

AAR10065

ID AAR10065 standard; protein; 553 AA.

XX AC AAR10065;

XX XX

DT 25-MAR-2003 (revised)

DT 14-MAR-1991 (first entry)

XX XX

DE Newcastle disease virus (NDV) F gene product.

XX KW

XX Avipoxvirus; fowlpoxvirus; vaccine.

XX OS

XX Newcastle disease virus.

XX PN

XX EP404576-A.

XX XX

PD 27-DEC-1990.

XX XX

PF 21-JUN-1990; 90EP-00306806.

XX XX

PR 22-JUN-1989; 89JP-00160157.

XX XX

PA (JAPG) NIPPON ZEON KK.

PA (SHIO) SHIONOGI & CO LTD.

XX (YANA/) YANAGIDA N.

PI Yangida N, Saeki S, Okawa S, Knamogawa K, Iritani Y, Sawaguchi K;

XX WPI: 1991-001591/01.

DR N-PSDB; AAR10060.

XX XX

PT Recombinant avipox virus - contg. CDNA coding for Newcastle disease virus in region non-essential for proliferation, used as live vaccine in fowls.

XX XX

PS Claim 3; Fig 3; 33pp; English.

XX XX

CC The sequence encoding the protein may be incorporated into a recombinant Avipoxvirus and used as a live vaccine in fowls, providing immunity to fowlpoxvirus and NDV. (Updated on 25-MAR-2003 to correct PA field.)

XX XX

SQ Sequence 553 AA;

Query Match

Best Local Similarity 98.8%; Score 2724; DB 2; Length 553;

Matches 544; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

QY

1 MGRSSTRIPVPLMLTVRVALSCVCTSSLDGRPLAAGIVTGDKAVNIYTSQTGS 60

1	MGSRSS	TRIE	FPVPL	MLTV	IRIM	LA	SCV	PT	SL	D	R	P	L	A	A	G	I	V	T	G	K	A	N	N	I	T	S	S	Q	T	G	S	60																										
61	II	V	K	L	P	N	M	P	K	D	E	A	C	A	P	L	E	A	N	R	T	L	T	T	P	L	G	D	S	I	R	I	Q	E	S	V	T	T	G	G	K	O	R	L	I	G	A	120											
61	III	K	L	P	N	M	P	K	D	E	A	C	A	P	L	E	A	N	R	T	L	T	T	P	L	G	D	S	I	R	I	Q	E	S	V	T	T	G	G	K	O	R	L	I	G	A	120												
121	II	G	A	A	L	G	V	A	T	A	A	I	T	A	S	A	L	I	Q	A	N	A	N	T	L	R	L	K	E	R	I	A	A	N	E	A	V	H	E	V	T	D	G	L	S	O	L	A	V	A	G	180							
121	II	G	V	A	L	G	V	A	T	A	A	I	T	A	S	A	L	I	Q	A	N	A	N	T	L	R	L	K	E	S	I	A	A	N	E	A	V	H	E	V	T	D	G	L	S	O	L	A	V	A	G	180							
181	K	M	O	F	V	N	D	O	F	N	K	T	A	E	L	D	C	I	K	I	T	O	Q	V	G	V	E	L	N	L	I	T	E	L	T	T	V	P	O	I	T	S	P	A	L	T	O	L	T	A	L	N	240						
181	K	M	O	F	V	N	D	O	F	N	K	T	A	E	L	D	C	I	K	I	T	O	Q	V	G	V	E	L	N	L	I	T	E	L	T	T	V	P	O	I	T	S	P	A	L	T	O	L	T	A	L	N	240						
241	L	A	G	N	M	D	Y	L	L	T	K	L	G	V	G	N	N	Q	L	S	L	I	G	S	L	I	T	C	N	P	I	L	D	S	O	T	O	L	L	G	I	Q	V	T	L	P	S	V	G	N	I	N	N	R	A	300			
241	L	A	G	N	M	D	Y	L	L	T	K	L	G	V	G	N	N	Q	L	S	L	I	G	S	L	I	T	C	N	P	I	L	D	S	O	T	O	L	L	G	I	Q	V	T	L	P	S	V	G	N	I	N	N	R	A	300			
301	T	L	E	T	L	S	V	T	T	K	F	A	S	A	L	P	V	K	V	T	T	G	S	V	I	E	L	D	T	S	C	I	E	T	D	L	D	I	C	T	R	I	V	T	F	P	M	S	P	G	I	360							
301	T	L	E	T	L	S	V	T	T	K	F	A	S	A	L	P	V	K	V	T	T	G	S	V	I	E	L	D	T	S	C	I	E	T	D	L	D	I	C	T	R	I	V	T	F	P	M	S	P	G	I	360							
361	S	C	L	S	G	N	T	S	A	C	M	Y	S	K	T	E	G	A	L	T	T	P	Y	M	L	K	G	S	V	I	A	N	C	K	M	T	T	C	R	A	D	P	P	G	I	I	S	O	N	Y	G	E	A	V	S	L	I	D	420
361	S	C	L	S	G	N	T	S	A	C	M	Y	S	K	T	E	G	A	L	T	T	P	Y	M	L	K	G	S	V	I	A	N	C	K	M	T	T	C	R	A	D	P	P	G	I	I	S	O	N	Y	G	E	A	V	S	L	I	D	420
421	R	O	S	C	N	V	I	S	L	D	G	I	T	L	R	S	G	E	F	A	T	Y	O	K	N	I	S	I	O	D	S	Q	V	I	V	T	G	N	L	D	I	S	T	E	L	G	N	V	N	N	I	S	N	A	L	D	K	480	
421	R	O	S	C	N	V	I	S	L	D	G	I	T	L	R	S	G	E	F	A	T	Y	O	K	N	I	S	I	O	D	S</																												

RESULT 2
ABR56236
ID ABR56236 standard: protein: 553 AA.

XX Disclosure; Fig 1; 22app; English.

XX

XX The present invention relates to a method (M1) for identifying a

CC candidate anti-viral agent (I), screening compounds and/or chemical

CC complexes for (I), modifying (I) to improve anti-viral activity, or

CC producing anti-viral agents, by generating a 3-dimensional structure

CC model of Respiratory Syncytial virus (RSV) Fusion (F)-protein with 3-

CC dimensional structure of target site to which an anti-viral agent may

CC interact and thus inhibit RSV-F protein activity. The present sequence is

CC with the Newcastle Disease Virus (NDV) F-protein used in a sequence alignment

CC with the RSV F-protein sequence (ABR56234)

XX

XX Sequence 553 AA:

SO

RESULT 3
ABR39678
ID ABR39678 standard: protein: 1103 AA.

```
OS Newcastle disease virus.
XX
XX
XX Key Location/Qualifiers
XX
XX Misc-difference 1..1103
XX
XX FT Protein
XX /note= "residues Xaa are encoded by internal stop codons"
XX 1..553
XX /note= "fusion glycoprotein (F)"
XX
XX PN WO2003022202-A2.
XX
XX PD 20-MAR-2003.
XX
XX PF 12-SEP-2002; 2002WO-IL000765.
XX
XX PR 12-SEP-2001; 2001IL-00145397.
XX
XX XX (YISS ) YISSUM RES & DEV CO.
XX PA (OVCU-) OVURE INC.
XX
XX PI Zakay-Rones Z, Panet A, Irving C;
XX
XX DR WPI: 2003-354498/33.
XX DR N-PSDB; ACC47077.
XX
XX PT Clonal lentogenic oncolytic strain, particularly a HUJ strain, of
XX FT Newcastle Disease Virus, useful for treating cancer, comprises a DNA
XX PT encoding a fusion gene and/or a hemagglutinin-neuraminidase gene.
XX
XX PS Example; Fig 10; 51pp; English.
XX
XX CC The invention relates to a clonal lentogenic oncolytic strain of
XX CC Newcastle Disease Virus (NDV) comprising a DNA sequence encoding for the
XX CC fusion glycoprotein (F) gene and a part of the haemagglutinin-
XX CC neuraminidase (HN) gene. The lentogenic oncolytic strain of NDV or a
XX CC viral glycoprotein having oncolytic activity, is useful in preparing a
XX CC composition for the treatment of cancer. The present sequence represents
XX CC a NDV strain HUJ amino acid sequence containing all of the F protein and
XX CC a partial HN protein
XX
XX SQ Sequence 1103 AA;

Query Match 95.0%; Score 2620; DB 6; Length 1103;
Best Local Similarity 93.7%; Pred. No. 2.8e-216;
Matches 518; Conservative 20; Mismatches 15; Indels 0; Gaps 0;

QY 1 MGRSSTRIPVPLMTVRVALALSCVPTSSLDGRPLAAGIVTGDKAVNIYTSSQTGS 60
DB 1 MGRPSTKNPAPMLTIRVALALSCICPANSIDGRPLAAGIVTGDKAVNIYTSSQTGS 60

QY 61 IIVKLLPNPKDEACAKAPLEAYNRTLTLLTPLGDSIRRIQESVTTSGGKQGRLLGA 120
DB 61 IIVKLLPNLPKDEACAKAPLDAYNRTLTLLTPLGDSIRRIQESVTTSGGKQGRLLGA 120

QY 121 IIGGALGVATAQITTAASALIOANQNAANILRLKERIAATNPAVHEVTDGLSQAVALG 180
DB 121 IIGGVALGVATAQITTAALALIOAKQNAANILRLKESIAATNPAVHEVTDGLSQAVALG 180

QY 181 KMOQFVNDOPNKTAQELDCIKITQOVGVENLYLTTLTVFGQIITSPLTQITIALYN 240
DB 181 KMOQFVNDOPNKTAQELDCIKITQOVGVENLYLTTLTVFGQIITSPLTQITIALYN 240

QY 241 LAGGNMDYLLTKLGVGNQNLSSLGSLITGNPLYDSOTQLAGIQTVLPSVGNLNMRA 300
DB 241 LAGGNMDYLLTKLGVGNQNLSSLGSLITGNPLYDSOTQLAGIQTVLPSVGNLNMRA 300

QY 301 TYLETLSVSTTKGFASALVPKVMKGVSVIEELDTSYCIETDLDLXCTRIVTFPMSPGIY 360
DB 301 TYLETLSVSTTRGFASALVPKVMKGVSVIEELDTSYCIETDLDLXCTRIVTFPMSPGIY 360

QY 361 SCLSGNTSACMSYKTEGALTTPMTLKGSVIANCKMTTCRCADPPGIIISQNYGEAVSLID 420
DB 361 SCLSGNTSACMSYKTEGALTTPMTLKGSVIANCKMTTCRCVNPFGIIISQNYGEAVSLID 420

QY 421 ROSCNVLSLGDITLRLSGEPDATYQKNISODSQTIVTGNLIDISTELGNVNSISNALDK 480
DB 421 KQSCNVLSLGGITLRLSGEDFTYQKNISQISQDSQVITITGNLIDISTELGNVNSISNALNK 480

QY 481 LEESNSKLDKVNKVLSTSTALITVLTSLVCGHLSLVLACVLMYKQKAAQKTLILWL 540
DB 481 LEESNRKLDKVNKVLSTSTALITVLTSLVCGHLSLVLACVLMYKQKAAQKTLILWL 540

QY 541 NNTLDQMRATTKM 553
DB 541 NNTLDQMRATTKM 553

RESULT 4
AA51231
ID AA51231 standard; protein; 553 AA.
XX
XX AC AA51231;
XX
XX DT 07-APR-2000 (first entry)
XX
XX DE Newcastle disease virus LaSota genome encoded protein 4.
XX
XX KW Avian-paramyxovirus; infection; lentogenic; F protein; vaccine;
XX KW respiratory disease; gastrointestinal disease; poultry pathogen;
XX KW local immunity.
XX
XX OS Newcastle disease virus.
XX
XX PN WO9966045-A1.
XX
XX PD 23-DEC-1999.
XX
XX PF 17-JUN-1999; 99WO-NL000377.
XX
XX PR 19-JUN-1998; 98EP-00202054.
XX
XX PA (DIEN-) STICHTING DIENST LANDBOUWKUNDIG ONDERZOE.
XX
XX PI Peeters BPH, De Leeuw OS, Koch G, Gielkens ALJ;
XX
XX WPI: 2000-106102/09.
XX
XX PT New avian paramyxovirus cDNA, useful for production of vaccine against
XX FT Newcastle disease virus.
XX
XX PS Disclosure; Fig 3; 115pp; English.
XX
XX CC This invention describes a novel avian-paramyxovirus cDNA (I) which
XX CC comprises a nucleic acid sequence corresponding to the 5' terminal end of
XX CC the genome of avian-paramyxovirus allowing the generation of an
XX CC infectious copy of avian-paramyxovirus. The cell line is useful for the
XX CC production of infectious lentogenic NDV (Newcastle Disease virus) without
XX CC the addition of exogenous lentogenic NDV (Newcastle Disease virus) to
XX CC generate a stable transfected cell line that expresses the wild-type F
XX CC protein in the virus envelope therefore providing infectious particles,
XX CC useful in the form of a vaccine, especially against respiratory and/or
XX CC gastrointestinal diseases. NDV can be easily cultured to very high titers
XX CC in embryonated eggs. Mass culture of embryonated eggs is relatively
XX CC cheap. NDV vaccines are relatively stable and can be simply administered
XX CC by mass application methods e.g. drinking water or by spraying or by
XX CC aerosol formation. The natural route of infection is by the respiratory
XX CC and/or gastrointestinal tract which are also the major routes of
XX CC infection of many other poultry pathogens. NDV can induce local immunity
XX CC despite the presence of circulating maternal antibody. This sequence
XX CC represents a protein encoded by the NDV strain LaSota genome which is
XX CC described in the method of the invention
XX
XX SQ Sequence 553 AA;

Query Match 94.9%; Score 2616; DB 3; Length 553;
Best Local Similarity 93.5%; Pred. No. 2e-216;
Matches 517; Conservative 20; Mismatches 16; Indels 0; Gaps 0;
```

New recombinant fowl pox virus for use in vaccines - contains genes expressing antigens of Newcastle disease virus and opt. infectious bronchitis virus.

Disclosure; Page 70-72; 85pp; English.

Newcastle Disease Virus (NDV) HN and F genes were inserted as a SfiI fragment into the homology vector 443-88.8 at the unique SfiI site. The fragment HN and F genes were inserted in the same transcriptional orientation as the ORF in the parental homology vector. The sequence of SfiI fragment is in AAQ68943/R58858/AAQ68945. The inserted SfiI fragment has the following structure: Junction A - Fragment 1 (HN, AAs 2-577) - Junction B - Fragment 2 (F, AAs 1-553) - Junction C - Fragment 3 (pBR322) - Junction D. Fragment 1 is approx. 1811 bp Avail to NaeI fragment of the NDV HN cDNA clone (B1 strain). Fragment 2 is an approx 1812 bp BamHI to PstI fragment of the full length NDV F cDNA (B1 Strain). Fragment 3 is an approx 235 bp PstI and ScaI fragment of the plasmid pBR322. The sequences of the junctions are in AAQ68945, AAQ68946, AAQ68947, Q68948. (Updated on 25-MAR-2003 to correct PN field.)

Sequence 553 AA;

Query Match 94.7%; Score 2610; DB 2; Length 553;
Best Local Similarity 93.1%; Pred. No. 6.7e-216;
Matches 515; Conservative 21; Mismatches 17; Indels 0; Gaps 0;

QY 1 MGRSSSTRIPVPLMLTVRVALALSCVPTSSLDGRPLAAAGIVTGDKAVNIYTSSTQGS 60
DB 1 MGRSPSTKNPAPMMLTIRVALVLSICIPANSIDGRPLAAAGIVTGDKAVNIYTSSTQGS 60
QY 61 IIVKLLPNMPKDEACAKAPLEAYNRTLTLLTPLGDSIRRIQESVTTSGGKQGRLLGA 120
DB 61 IIVKLLPNMPKDEACAKAPLEAYNRTLTLLTPLGDSIRRIQESVTTSGGKQGRLLGA 120
QY 121 IIGGAALGVATAAQAQITTAASALIQAQNAANILRLKESIAATNEAVHEVTDGLSOLAVAG 180
DB 121 IIGGVALGVATAAQAQITTAASALIQAQNAANILRLKESIAATNEAVHEVTDGLSOLAVAG 180
QY 181 KMQQFVNDQFNKTAQELDCIKITQGVGVELNLYLTTELTVFGPQITSALQTQTALYN 240
DB 181 KMQQFVNDQFNKTAQELDCIKITQGVGVELNLYLTTELTVFGPQITSALQTQTALYN 240
QY 241 LAGGNDYLLTKLGVGNQSLIGSLITGNPILYDSQTLGLGIVTLPVSGNLNNMRA 300
DB 241 LAGGNDYLLTKLGVGNQSLIGSLITGNPILYDSQTLGLGIVTLPVSGNLNNMRA 300
QY 301 TYLETSLVSTTKGFASALVPKVMKGVSVIELDTSYCIETDLDLYCTRIVTFPMSPGIY 360
DB 301 TYLETSLVSTTRGFASALVPKVMKGVSVIELDTSYCIETDLDLYCTRIVTFPMSPGIY 360
QY 361 SCLSGNTSACMYSKTEGALTTPYMTIKGSVIANCKMTTCRCADPPGIISQNYGEAVSLID 420
DB 361 SCLSGNTSACMYSKTEGALTTPYMTIKGSVIANCKMTTCRCVNPFGIISQNYGEAVSLID 420
QY 421 RQSCNVLSDGTTLRSLGFEFATYQKNISIQDSQVIVTGNLIDISTELGNVNNISNALDK 480
DB 421 RQSCNVLSDGTTLRSLGFEFATYQKNISIQDSQVIVTGNLIDISTELGNVNNISNALNK 480
QY 481 LEESNRKLDKVNKLSTSTALITYVLTVISLVCGILSLVACYLIMYKQKQOQKTLMLWG 540
DB 481 LEESNRKLDKVNKLSTSTALITYVLTVISLVCGILSLVACYLIMYKQKQOQKTLMLWG 540
QY 541 NNTLDQMRATTKM 553
DB 541 NNTLDQMRATTKM 553

RESULT 6
ID AAR49141
ID AAR49141 standard; protein; 553 AA.
XX AC AAR49141;
XX AC

QY 1 MGRSSSTRIPVPLMLTVRVALALSCVPTSSLDGRPLAAAGIVTGDKAVNIYTSSTQGS 60
DB 1 MGRSPSTKNPAPMMLTIRVALVLSICIPANSIDGRPLAAAGIVTGDKAVNIYTSSTQGS 60
QY 61 IIVKLLPNMPKDEACAKAPLEAYNRTLTLLTPLGDSIRRIQESVTTSGGKQGRLLGA 120
DB 61 IIVKLLPNMPKDEACAKAPLEAYNRTLTLLTPLGDSIRRIQESVTTSGGKQGRLLGA 120
QY 121 IIGGAALGVATAAQAQITTAASALIQAQNAANILRLKESIAATNEAVHEVTDGLSOLAVAG 180
DB 121 IIGGVALGVATAAQAQITTAASALIQAQNAANILRLKESIAATNEAVHEVTDGLSOLAVAG 180
QY 181 KMQQFVNDQFNKTAQELDCIKITQGVGVELNLYLTTELTVFGPQITSALQTQTALYN 240
DB 181 KMQQFVNDQFNKTAQELDCIKITQGVGVELNLYLTTELTVFGPQITSALQTQTALYN 240
QY 241 LAGGNDYLLTKLGVGNQSLIGSLITGNPILYDSQTLGLGIVTLPVSGNLNNMRA 300
DB 241 LAGGNDYLLTKLGVGNQSLIGSLITGNPILYDSQTLGLGIVTLPVSGNLNNMRA 300
QY 301 TYLETSLVSTTKGFASALVPKVMKGVSVIELDTSYCIETDLDLYCTRIVTFPMSPGIY 360
DB 301 TYLETSLVSTTRGFASALVPKVMKGVSVIELDTSYCIETDLDLYCTRIVTFPMSPGIY 360
QY 361 SCLSGNTSACMYSKTEGALTTPYMTIKGSVIANCKMTTCRCADPPGIISQNYGEAVSLID 420
DB 361 SCLSGNTSACMYSKTEGALTTPYMTIKGSVIANCKMTTCRCVNPFGIISQNYGEAVSLID 420
QY 421 RQSCNVLSDGTTLRSLGFEFATYQKNISIQDSQVIVTGNLIDISTELGNVNNISNALDK 480
DB 421 RQSCNVLSDGTTLRSLGFEFATYQKNISIQDSQVIVTGNLIDISTELGNVNNISNALNK 480
QY 481 LEESNRKLDKVNKLSTSTALITYVLTVISLVCGILSLVACYLIMYKQKQOQKTLMLWG 540
DB 481 LEESNRKLDKVNKLSTSTALITYVLTVISLVCGILSLVACYLIMYKQKQOQKTLMLWG 540
QY 541 NNTLDQMRATTKM 553
DB 541 NNTLDQMRATTKM 553

RESULT 5
AAR58858
ID AAR58858 standard; protein; 553 AA.
AC AC
AC AAR58858;
DT 25-MAR-2003 (revised)
DT 13-APR-1995 (first entry)
XX Newcastle Disease Virus F gene product.
XX SfiI fragment; Newcastle Disease Virus; F gene.
XX Synthetic.
XX WO9419014-A1.
XX 01-SEP-1994.
XX 28-FEB-1994; 94WO-US0001826.
XX 26-FEB-1993; 93US-00024156.
XX (SYTR) SYNTRO CORP.
XX (JAPG) NIPPON ZEON KK.
XX Cochran MD;
XX WPI; 1994-294007/36.
XX N-PSDB; AAQ68943.


```

XX avian influenza; recombinant poultry virus vaccine; HVT;
KW Turkey Herpes Virus.
XX Newcastle disease virus (STRAIN TEXAS).
OS EP447303-A.
XX 18-SEP-1991.
XX 07-MAR-1991; 91EP-00400634.
XX 12-MAR-1990; 90FR-00003105.
XX (INMR ) RHONE MERIEUX SA.
XX Reysenelon A, Kohen G;
PI WPI; 1991-275886/38.
XX N-PSDB; AAQ13668.
XX New herpes recombinants - useful as vaccines against human and animal
PT viral conditions, e.g. fowlpest, coccidiosis and pasteurellosis, etc.
XX Example 3; Page 17-19; 22pp; French.
XX This sequence is an immunogenic Newcastle Disease Virus fusion protein.
CC It can be inserted into the RR2 (ribonucleotide reductase small subunit)
CC gene of the Turkey Herpes Virus. The HVT is suitable for use in live
CC vaccines as it is apathogenic and non-oncogenic. Other vaccines are
CC constructed in a similar way using immunogens which protect against e.g.
CC avian infectious bronchitis, colibacillosis, Marek Disease, Gumboro
CC Disease, avian anaemia, etc. See also AAQ13430. (Updated on 25-MAR-2003
CC to correct PA field.) (Updated on 25-MAR-2003 to correct PI field.)
CC (Updated on 27-AUG-2003 to correct OS field.)
XX
SQ Sequence 553 AA;

Query Match          94.5%; Score 2606; DB 2; Length 553;
Best Local Similarity 94.8%; Pred. No. 1.5e-215;
Matches 524; Conservative 9; Mismatches 20; Indels 0; Gaps 0;

QY 1 MGRSSTRIPVPLMLTVRVALALSCVCPSTSSLDGRPLAAAGIVTGDKAVNIYTSQTGS 60
DB 1 MGRSSTRIPVPLMLTIRALTLSCLRTSSLDGRPLAAAGIVTGDKAVNIYTSQTGS 60
QY 61 IIVKLLPNMPKDEKACAPLEAYNRTLTLLPLGDSIRRIQESVTTSGGKQRLIGA 120
DB 61 IIVKLLPNMPKDEKACAPLEAYNRTLTLLPLGDSIRRIQESVTTSGGRRQRRFIGA 120
QY 121 IIGGAALGVATAAQITTAASALICANONANILKRIATNEAVHEVTDGLSOLAVAG 180
DB 121 IIGSVALGVATAAQITTAASALICANONANILKESIAATNEAVHEVTDGLSOLAVAG 180
QY 181 KMQQFVNDQFNKTAQELDCIKITQQGVVELNLYLTETLVFGQITSPALTQTITQALYN 240
DB 181 KMQQFVNDQFNNTAQELDCIKIAQQGVVELNLYLTETLVFGQITSPALTQTITQALYN 240
QY 241 LAGGNMDYLLTKLGVGNQNLSSLIGSLITGNPILYDSQTQLLGIQVTLPSVGNLNMRA 300
DB 241 LAGGNMDYLLTKLGVGNQNLSSLIGSLITGNPILYDSQTQLLGIQVTLPSVGNLNMRA 300
QY 301 TYLETLSVSTTKGFASALVPKVMKGVSVIEELDTSCYIETDLDLYCTRIVTPMSPGIY 360
DB 301 TYLETLSVSTTKGFASALVPKVMKGVSVIEELDTSCYIETDLDLYCTRIVTPMSPGIY 360
QY 361 SCLSGNTSACMYSKTEGALTTPYMLTKSGVIANCKMTTCRCADPPGLISQNYGEAVSLID 420
DB 361 SCLSGNTSACMYSKTEGALTTPYMLTKSGVIANCKMTTCRCADPPGLISQNYGEAVSLID 420
QY 421 ROSCNVSLDGIITRLSGEFDATYQKNI SIQDSQVI VTGNL D I STELGNVNNISNALDK 480
DB 421 RHSCNVSLDGIITRLSGEFDATYQKNI SILD SQVI VTGNL D I STELGNVNNISNALNK 480

QY 481 LEESNSKLDKVNKLTSTSTALITVIVLTISLVGILSLVACLYMYKQKQAQKTLMLG 540
DB 481 LEESNSKLDKVNKLTSTSTALITVIVLTISLVGILSLVACLYMYKQKQAQKTLMLG 540
QY 541 NNTLDQWRATTKM 553
DB 541 NNTLDQWRATTKI 553

RESULT 13
AAW44941
ID AAW44941 standard; protein; 553 AA.
XX
AC AAW44941;
XX
DT 28-OCT-1998 (first entry)
XX
DE Newcastle disease virus glycoprotein F.
XX
KW Multivalent vaccine; bird; pathogen; respiratory disease; MDV; NDV; IBDV;
KW digestive disease; Marek's disease virus; Newcastle disease virus; CAV;
KW infectious bursal disease virus; Gumboro disease virus; vaccine; ILTV;
KW avian infectious bronchitis virus; IBV; chicken anaemia virus; AEV; PCR;
KW infectious laryngotracheitis virus; avian encephalomyelitis virus; TRTV;
KW turkey rhinotracheitis virus; influenza virus A avian; vector; primer;
KW amplification; glycoprotein; gallid herpesvirus.
XX
OS Newcastle disease virus.
XX
PN FR2751225-A1.
XX
PD 23-JAN-1998.
XX
PF 19-JUL-1996; 96FR-00009339.
XX
PR 19-JUL-1996; 96FR-00009339.
XX
PA (INMR ) RHONE MERIEUX SA.
XX
PI Audonnet JCF, Bouchardon A, Riviere MEA;
XX
DR WPI; 1998-112825/11.
DR N-PSDB; AAW49342.
XX
PT Multi-valent polynucleotide vaccines against avian pathogens - consist of
PT at least 3 plasmids able to express protective antigens from specified
PT viruses.
XX
PS Example 10; Fig 6; 55pp; French.
XX
CC The invention relates to a multivalent vaccine for protecting birds
CC against several pathogens, especially pathogens associated with
CC respiratory and digestive diseases. The pathogens are especially selected
CC from Marek's disease virus (MDV), Newcastle disease virus (NDV),
CC infectious bursal disease virus (IBDV), avian infectious bronchitis virus
CC (IBV), chicken anaemia virus (CAV), infectious laryngotracheitis virus
CC (ILT), avian encephalomyelitis virus (AEV), turkey rhinotracheitis virus
CC (TRTV) and influenza virus A avian (AIV). The vaccines are preferably
CC composed of polynucleotide sequences encoding 3 antigens, all as part of
CC vectors. This sequence represents the NDV strain Texas GB glycoprotein F.
CC The coding sequence was subcloned into the plasmid pVR1012 to generate
CC plasmid pAB047 for use in the vaccine
XX
SQ Sequence 553 AA;

Query Match          94.5%; Score 2606; DB 2; Length 553;
Best Local Similarity 94.8%; Pred. No. 1.5e-215;
Matches 524; Conservative 9; Mismatches 20; Indels 0; Gaps 0;

QY 1 MGRSSTRIPVPLMLTVRVALALSCVCPSTSSLDGRPLAAAGIVTGDKAVNIYTSQTGS 60
DB 1 MGRSSTRIPVPLMLTIRALTLSCLRTSSLDGRPLAAAGIVTGDKAVNIYTSQTGS 60
QY 61 IIVKLLPNMPKDEKACAPLEAYNRTLTLLPLGDSIRRIQESVTTSGGKQRLIGA 120
DB 61 IIVKLLPNMPKDEKACAPLEAYNRTLTLLPLGDSIRRIQESVTTSGGRRQRRFIGA 120
QY 121 IIGGAALGVATAAQITTAASALICANONANILKRIATNEAVHEVTDGLSOLAVAG 180
DB 121 IIGSVALGVATAAQITTAASALICANONANILKESIAATNEAVHEVTDGLSOLAVAG 180
QY 181 KMQQFVNDQFNKTAQELDCIKITQQGVVELNLYLTETLVFGQITSPALTQTITQALYN 240
DB 181 KMQQFVNDQFNNTAQELDCIKIAQQGVVELNLYLTETLVFGQITSPALTQTITQALYN 240
QY 241 LAGGNMDYLLTKLGVGNQNLSSLIGSLITGNPILYDSQTQLLGIQVTLPSVGNLNMRA 300
DB 241 LAGGNMDYLLTKLGVGNQNLSSLIGSLITGNPILYDSQTQLLGIQVTLPSVGNLNMRA 300
QY 301 TYLETLSVSTTKGFASALVPKVMKGVSVIEELDTSCYIETDLDLYCTRIVTPMSPGIY 360
DB 301 TYLETLSVSTTKGFASALVPKVMKGVSVIEELDTSCYIETDLDLYCTRIVTPMSPGIY 360
QY 361 SCLSGNTSACMYSKTEGALTTPYMLTKSGVIANCKMTTCRCADPPGLISQNYGEAVSLID 420
DB 361 SCLSGNTSACMYSKTEGALTTPYMLTKSGVIANCKMTTCRCADPPGLISQNYGEAVSLID 420
QY 421 ROSCNVSLDGIITRLSGEFDATYQKNI SIQDSQVI VTGNL D I STELGNVNNISNALDK 480
DB 421 RHSCNVSLDGIITRLSGEFDATYQKNI SILD SQVI VTGNL D I STELGNVNNISNALNK 480

```

QY 61 IIVKLLNMPKDEKACAKAPLEAYNRITLTLLTPLGDSIRRIQESVTTSGGKQGRLLGA 120
Db 61 IIVKLLNMPKDEKACAKAPLEAYNRITLTLLTPLGDSIRRIQESVTTSGGKQGRLLGA 120
QY 121 IIGGAALGVATAAQTAAASALIQANONAAANILRLKERIAATNEAVHEVTDGLSOLAVAG 180
Db 121 IIGGAALGVATAAQTAAASALIQANONAAANILRLKERIAATNEAVHEVTDGLSOLAVAG 180
QY 181 KMQGFVNDQFNKTAQELDCIKITQQGVGVELNLYLTTELTTVFGPQITSPALTIQALYN 240
Db 181 KMQGFVNDQFNKTAQELDCIKITQQGVGVELNLYLTTELTTVFGPQITSPALTIQALYN 240
QY 241 LAGNMNDYLLTKLGVGNQSLIGSLITGNPILYDSOTQLLGIQVTLPSVGNLNNMRA 300
Db 241 LAGNMNDYLLTKLGVGNQSLIGSLITGNPILYDSOTQLLGIQVTLPSVGNLNNMRA 300
QY 301 TYLETSLVSTTKGFASALVPKVMKGVSVIEBELDTSYCIETDLDLYCTRIVTFPMSPGIY 360
Db 301 TYLETSLVSTTKGFASALVPKVMKGVSVIEBELDTSYCIETDLDLYCTRIVTFPMSPGIY 360
QY 361 SCLSGNTSACMSYKTEGALTTPYMTLKGSVIANCKMTTCRCADPPGIISQNYGEAVSLID 420
Db 361 SCLSGNTSACMSYKTEGALTTPYMTLKGSVIANCKMTTCRCADPPGIISQNYGEAVSLID 420
QY 421 ROSCNVLSLDGITLRLSGEPDATYQKNISIODSQVIVTGNLIDISTELGNVNNISNALDK 480
Db 421 ROSCNVLSLDGITLRLSGEPDATYQKNISIODSQVIVTGNLIDISTELGNVNNISNALDK 480
QY 481 LEESNKLKDVNKLVTSTALITYIVLTIVSLVCGILSLVACVLMYKQKQAKQKTLMLG 540
Db 481 LEESNKLKDVNKLVTSTALITYIVLTIVSLVCGILSLVACVLMYKQKQAKQKTLMLG 540
QY 541 NNTLDQMRATTKM 553
Db 541 NNTLDQMRATTKI 553
RESULT 14
AAP70176
ID AAP70176 standard; protein; 553 AA.
XX AC
XX AAP70176;
XX 27-AUG-2003 (revised)
DT 25-MAR-2003 (revised)
DT 03-APR-1991 (first entry)
XX DE
XX Sequence of Newcastle Disease Virus (NDV) F polypeptide.
XX Epitope; probe; diagnosis.
XX Newcastle disease virus.
XX EP227414-A.
XX 01-JUL-1987.
XX 16-DEC-1986; 86EP-00309804.
XX 18-DEC-1985; 85GB-00031147.
XX 14-APR-1986; 86GB-00009037.
XX 15-JUL-1986; 86US-00885765.
XX (NATR) NAT RES DEV CORP.
XX Bingham RW, Chambers P, Emmerson PT, Millar NS;
XX WPI; 1987-179630/26.
XX N-PSDB; AAN70261.
XX Newcastle disease virus gene clones - comprise polynucleotide(s) encoding
PT the HN and/or F protein of Newcastle disease virus RNA.

XX PS
XX Example; Page 11-16; 22pp; English.
CC An artificial polynucleotide encoding an HN and/or F polypeptide of
CC Newcastle Disease Virus (NDV) DNA, a bioprecursor of the polypeptide, or
CC an epitopic portion of the polypeptide or an artificial nucleotide
CC complementary to the polynucleotide are claimed. The polynucleotides are
CC useful for preparing a probe for extracting similar genes from a gene
CC library or for identifying the presence of NDV virions in a sample obcd.
CC from poultry. (Updated on 25-MAR-2003 to correct PA field.) (Updated on
CC 27-AUG-2003 to correct OS field.)
SQ Sequence 553 AA;
Query Match 94.4%; Score 2603; DB 1; Length 553;
Best Local Similarity 93.5%; Pred. No. 2.7e-215; Indels 0; Gaps 0;
Matches 517; Conservative 19; Mismatches 17;
QY 1 MGRSRSTRIPVPLMLTVRVALALSCVCTPSLDGRPLAAAGIVVTGKAVNIYTSQTGS 60
Db 1 MGRPSRTKNPVPVMTLTVRVALVLSICIPANSIDGRPLAAAGIVVTGKAVNIYTSQTGS 60
QY 61 IIVKLLNMPKDEKACAKAPLEAYNRITLTLLTPLGDSIRRIQESVTTSGGKQGRLLGA 120
Db 61 IIVKLLNMPKDEKACAKAPLEAYNRITLTLLTPLGDSIRRIQESVTTSGGKQGRLLGA 120
QY 121 IIGGAALGVATAAQTAAASALIQANONAAANILRLKERIAATNEAVHEVTDGLSOLAVAG 180
Db 121 IIGGAALGVATAAQTAAASALIQANONAAANILRLKERIAATNEAVHEVTDGLSOLAVAG 180
QY 181 KMQGFVNDQFNKTAQELDCIKITQQGVGVELNLYLTTELTTVFGPQITSPALTIQALYN 240
Db 181 KMQGFVNDQFNKTAQELDCIKITQQGVGVELNLYLTTELTTVFGPQITSPALTIQALYN 240
QY 241 LAGNMNDYLLTKLGVGNQSLIGSLITGNPILYDSOTQLLGIQVTLPSVGNLNNMRA 300
Db 241 LAGNMNDYLLTKLGVGNQSLIGSLITGNPILYDSOTQLLGIQVTLPSVGNLNNMRA 300
QY 301 TYLETSLVSTTKGFASALVPKVMKGVSVIEBELDTSYCIETDLDLYCTRIVTFPMSPGIY 360
Db 301 TYLETSLVSTTKGFASALVPKVMKGVSVIEBELDTSYCIETDLDLYCTRIVTFPMSPGIY 360
QY 361 SCLSGNTSACMSYKTEGALTTPYMTLKGSVIANCKMTTCRCADPPGIISQNYGEAVSLID 420
Db 361 SCLSGNTSACMSYKTEGALTTPYMTLKGSVIANCKMTTCRCADPPGIISQNYGEAVSLID 420
QY 421 ROSCNVLSLDGITLRLSGEPDATYQKNISIODSQVIVTGNLIDISTELGNVNNISNALDK 480
Db 421 ROSCNVLSLDGITLRLSGEPDATYQKNISIODSQVIVTGNLIDISTELGNVNNISNALDK 480
QY 481 LEESNKLKDVNKLVTSTALITYIVLTIVSLVCGILSLVACVLMYKQKQAKQKTLMLG 540
Db 481 LEESNKLKDVNKLVTSTALITYIVLTIVSLVCGILSLVACVLMYKQKQAKQKTLMLG 540
QY 541 NNTLDQMRATTKM 553
Db 541 NNTLDQMRATTKM 553
RESULT 15
ABG31709
ID ABG31709 standard; protein; 564 AA.
XX AC
XX ABG31709;
XX 15-NOV-2002 (first entry)
XX Newcastle disease virus (NDV) fusion protein.
XX DE
XX Newcastle disease virus; NDV; novel recombinant avian herpesvirus; NAHV;
XX KW herpes virus of turkeys; HVT; Marek's disease; Newcastle disease;
XX KW infectious laryngotracheitis; virucide; immunostimulant; vaccine.
XX

OS	Newcastle disease virus.		
XX			
FH	Key	Location/Qualifiers	
FT	Misc-difference 54	/label= unknown	
FT		/note= "Encoded by CTN"	
FT			
XX			
PN	US2002081316-A1.		
XX			
PD	27-JUN-2002.		
XX			
PF	14-JUN-2001; 2001US-00881457.		
XX			
PR	12-JUN-1992; 92US-00898087.		
PR	26-FEB-1993; 93US-00023610.		
PR	14-JUN-1993; 93WO-US005681.		
PR	09-AUG-1994; 94US-00288065.		
PR	09-AUG-1995; 95WO-US010245.		
PR	13-JUN-1996; 96US-00663566.		
PR	21-FEB-1997; 97US-00804372.		
PR	25-OCT-1999; 99US-00426352.		
XX			
PA	(COCH/) COCHRAN M D.		
PA	(COOK/) COOK S M.		
PA	(WILD/) WILD M A.		
XX			
PI	Cochran MD, Cook SM, Wild MA;		
XX			
DR	WPI; 2002-635456/68.		
DR	N-PSDB; ABK90556.		
XX			
PT	Novel recombinant avian herpesvirus comprising unique long and repeat		
PT	viral genome regions of herpes virus of turkeys, unique short viral		
PT	genome region of Marek's disease virus, and optional foreign DNA		
PT	sequence.		
XX			
PS	Disclosure; Page 14-16; 26pp; English.		
XX			
CC	The invention relates to a novel recombinant avian herpesvirus (NAHV)		
CC	comprising a herpes virus of turkeys (HVT) unique long (UL) and repeat		
CC	viral genome region and a Marek's disease virus unique short (US) viral		
CC	genome region where at least one foreign DNA sequence is inserted within		
CC	a US2 gene of the US region of the NAHV, and is capable of being		
CC	expressed in a host cell. NAHV is useful for producing vaccines used for		
CC	immunising an avian species against Newcastle disease, infectious		
CC	laryngotracheitis and Marek's disease. This sequence represents a		
CC	Newcastle disease virus (NDV) fusion protein		
XX			
SQ	Sequence 564 AA;		
Query Match 90.4%; Score 2493.5; DB 5; Length 564;			
Best Local Similarity 89.7%; Pred. No. 7.8e-206;			
Matches 496; Conservative 24; Mismatches 32; Indels 1; Gaps 1;			
QY	1	MGSRSTRIPVPLMTVRVALALSCVCPSSLDGRPLAAGIVVTGDKAVNIYTSQTGS	60
Db	13	MGSRPTKTPAPMMLIRVALVLSCLCPANSIDGRPLAAGXWLQETKQ-STYTPHPRQV	71
QY	61	IIVKLLPNMPKDEACAKAPLEAYNRTLTLTFLGDSIRRIQESVTTSGGKQGRLLGA	120
Db	72	NHIKLLPNLPKDEACAKAPLDAYNRTLTLTFLGDSIRRIQESVTTSGGKQGRLLGA	131
QY	121	IIGGAALGVATAAQITAAALIOANQNANILRLKERIAATNEAVHEVTDGLSQLAVAG	180
Db	132	IIGVALGVATAAQITAAAALIOAKQNAANILRLKESIAATNEAVHEVTDGLSQLAVAG	191
QY	181	KMQQFVNDQNKTAQELDCIKITQQVGVELNLYLTTLTVFGPQITSPALTLTIOALYN	240
Db	192	KMQQFVNDQNKTAQELDCIKIAQQVGVELNLYLTSTTVFGPQITSPALKLTIQALYN	251
QY	241	LAGNMDYLLTKLGVGNQLSSLIGSLITGNPILYDSOTQLLGIOVTLPSVGNLNMRA	300
Db	252	LAGNMDYLLTKLIGGNQLSSLIGSLITGNPILYDSOTQLLGIOVTLPSVGNLNMRA	311

QY	301	TYLETLSVSTTKGFASALVPKVMKVGSVIEELDTSYCIETDLDLCTRIIVTPMSPGIY	360
Db	312	TYLETLSVSTTKGFASALVPKVMKVGSVIEELDTSYCIETDLDLCTRIIVTPMSPGIY	371
QY	361	SCLSGNTSACMYSKTEGALTTPYMTLKGSVIANCKMTTCRCADPPGIIISQNYGEAVSLID	420
Db	372	SCLSGNTSACMYSKTEGALTTPYMTLKGSVIANCKMTTCRCVNPPIISQNYGEAVSLID	431
QY	421	RQSCNVLSLDGITRLSGFEDATYQKNISIQDSQVIVTGNLDISTELGNVNNISNALDK	480
Db	432	KQSCNVLSLGGITRLSGFEDVYQKNISIQDSQVITGNLDISTELGNVNNISNALNK	491
QY	481	LEESNKLDKVNKLTSTTSALITYIVLTVISLVCGILSLVLACILMYKAKOQKTLWLIG	540
Db	492	LEESNRKLDKVNKLTSTTSALITYIVLTVISLVFGILSLILACILMYKAKOQKTLWLIG	551
QY	541	NNTLDQMRATTKM	553
Db	552	NNTLDQMRATTKM	564

Search completed: April 18, 2004, 01:23:38
Job time : 103 secs

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Result No.	Score	Query		DB	ID	Description
		Match	Length			
1	2610	94.7	553	2	US-08-663-566A-13	Sequence 13, Appl
2	2610	94.7	553	2	US-08-484-575A-14	Sequence 14, Appl
3	2610	94.7	553	2	US-08-023-610-13	Sequence 13, Appl
4	2610	94.7	553	2	US-08-288-065A-13	Sequence 13, Appl
5	2610	94.7	553	2	US-08-362-240A-13	Sequence 13, Appl
6	2610	94.7	553	3	US-08-477-459-14	Sequence 14, Appl
7	2610	94.7	553	3	US-08-479-869-14	Sequence 14, Appl
8	2610	94.7	553	3	US-08-486-414-14	Sequence 14, Appl
9	2610	94.7	553	3	US-08-804-372A-11	Sequence 11, Appl
10	2610	94.7	553	5	PCT-US94-01826A-11	Sequence 11, Appl
11	2610	94.7	553	5	PCT-US94-02252A-14	Sequence 14, Appl
12	2610	94.7	553	5	PCT-US95-10245-13	Sequence 13, Appl
13	2572	93.3	553	6	5310678-1	Patent No. 5310678
14	2086.5	75.7	436	3	US-08-486-099-94	Sequence 94, Appl
15	2086.5	75.7	436	3	US-08-360-107A-104	Sequence 104, Appl
16	2086.5	75.7	436	3	US-08-484-223B-94	Sequence 94, Appl
17	2086.5	75.7	436	3	US-08-919-597-94	Sequence 94, Appl
18	2086.5	75.7	436	3	US-08-475-668A-94	Sequence 94, Appl
19	2086.5	75.7	436	3	US-08-485-551A-94	Sequence 94, Appl
20	2086.5	75.7	436	3	US-08-471-913A-94	Sequence 94, Appl
21	2086.5	75.7	436	3	US-08-485-264A-94	Sequence 94, Appl
22	2086.5	75.7	436	4	US-08-474-349A-94	Sequence 94, Appl
23	2086.5	75.7	436	4	US-08-475-208A-30	Sequence 30, Appl
24	2086.5	75.7	436	4	US-08-470-896-94	Sequence 94, Appl
25	2086.5	75.7	436	4	US-08-485-546A-94	Sequence 94, Appl
26	712	25.8	551	2	US-08-700-548-4	Sequence 4, Appl
27	689	25.0	542	1	US-08-321-587-2	Sequence 2, Appl

Query Match

Best Local Similarity

Matches

94.7%

Score 2610;

DB 2;

Length 553;

93.1%

Pred. No. 3,2e-230;

21;

Mismatches 17;

Indels 0;

Gaps 0;

Qy

1

MGSRSTRIPVPLMLTVRVALALSCVPTSLDGRPLAAAGIVVTGDKAVNIYTSQTGS

60

Db

1

MGSRPSTKNPAPMWLTIRVALVLSICIPANSIDGRPLAAAGIVVTGDKAVNIYTSQTGS

60

Qy

61

IIVKLLPNMKDEACAKAPLEAYNRLTLLPLGDSIRRIQSVTTSGGKGRIGLA

120

Db

61

IIVKLLPNMKDEACAKAPLEAYNRLTLLPLGDSIRRIQSVTTSGGKGRIGLA

120

Qy

121

IIGAAALGVATAAQITAAASALIOANQNAANILRLKERIAATNEAVHEVTDGLSLAVAVG

180

Db

121

IIGVALGVATAAQITAAALIQAKQNAANILRLKESIAATNEAVHEVTDGLSLAVAVG

180

Qy

181

KMQQFVNDQFNKTAQELDCIKITQOVGVNELNLYLTELTTVFGPOITSPALTIQALYN

240

Db

181

KMQQFVNDQFNKTAQELDCIKIAQQVGVNELNLYLTESTTTFGPOITSPALNKLTIOALYN

240

Qy

241

LAGNMVLLTKLGVGNQSSLLGSLITGNPILYDSOTOLLGIVQVTLPSVGNLNNRA

300

Db

241

LAGNMVLLTKLGVGNQSSLLGSLITGNPILYDSOTOLLGIVQVTLPSVGNLNNRA

300

Qy

301

TYLETLVSVTTKGFASALVPKVMKGVSVIEELDTSYCIETDLDLYCTRIVTFPMSPGIY

360

Db

301

TYLETLVSVTTRGFASALVPKVMKGVSVIEELDTSYCIETDLDLYCTRIVTFPMSPGIY

360

Qy

361

SCLSGNTSACMYSTEGALTPPYMTLKGSVIANCKMTTCRCADPPGIISQNYGEAVSLID

420

Db

361

SCLSGNTSACMYSTEGALTPPYMTIKGSVIANCKMTTCRCVNPPIISQNYGEAVSLID

420

Qy

421

ROSCNVLSLGGITLRLSGERDATYQKNISIODSVIVTGNLDISTELGNVNNISNALDK

480

Db

421

KOSCNVLSLGGITLRLSGEFDTYQKNISIODSVIITGNLDISTELGNVNNISNALNK

480

Qy

481

LEENSKLDKVNKLTSTALITYIVLTVISLVCGILSLVLACVLMYKOKAQKTLMLWG

540

Db

481

LEENSKLDKVNKLTSTALITYIVLTVIISLVFGILSLILACVLMYKOKAQKTLMLWG

540

Qy

541

NNTLDQMRATTKM

553

Db

541

NNTLDQMRATTKM

553

Query Match

Best Local Similarity

Matches

94.7%

Score 2610;

DB 2;

Length 553;

93.1%

Pred. No. 3,2e-230;

21;

Mismatches 17;

Indels 0;

Gaps 0;

Qy

1

MGSRSTRIPVPLMLTVRVALALSCVPTSLDGRPLAAAGIVVTGDKAVNIYTSQTGS

60

Db

1

MGSRPSTKNPAPMWLTIRVALVLSICIPANSIDGRPLAAAGIVVTGDKAVNIYTSQTGS

60

Qy

61

IIVKLLPNMKDEACAKAPLEAYNRLTLLPLGDSIRRIQSVTTSGGKGRIGLA

120

Db

61

IIVKLLPNMKDEACAKAPLEAYNRLTLLPLGDSIRRIQSVTTSGGKGRIGLA

120

Qy

121

IIGAAALGVATAAQITAAASALIOANQNAANILRLKERIAATNEAVHEVTDGLSLAVAVG

180

Db

121

IIGVALGVATAAQITAAALIQAKQNAANILRLKESIAATNEAVHEVTDGLSLAVAVG

180

Qy

181

KMQQFVNDQFNKTAQELDCIKITQOVGVNELNLYLTELTTVFGPOITSPALTIQALYN

240

Db

181

KMQQFVNDQFNKTAQELDCIKIAQQVGVNELNLYLTESTTTFGPOITSPALNKLTIOALYN

240

Qy

241

LAGNMVLLTKLGVGNQSSLLGSLITGNPILYDSOTOLLGIVQVTLPSVGNLNNRA

300

Db

241

LAGNMVLLTKLGVGNQSSLLGSLITGNPILYDSOTOLLGIVQVTLPSVGNLNNRA

300

Qy

301

TYLETLVSVTTKGFASALVPKVMKGVSVIEELDTSYCIETDLDLYCTRIVTFPMSPGIY

360

Db

301

TYLETLVSVTTRGFASALVPKVMKGVSVIEELDTSYCIETDLDLYCTRIVTFPMSPGIY

360

Qy

361

SCLSGNTSACMYSTEGALTPPYMTLKGSVIANCKMTTCRCADPPGIISQNYGEAVSLID

420

Db

361

SCLSGNTSACMYSTEGALTPPYMTIKGSVIANCKMTTCRCVNPPIISQNYGEAVSLID

420

Qy

421

ROSCNVLSLGGITLRLSGERDATYQKNISIODSVIVTGNLDISTELGNVNNISNALDK

480

Db

421

KOSCNVLSLGGITLRLSGEFDTYQKNISIODSVIITGNLDISTELGNVNNISNALNK

480

Qy

481

LEENSKLDKVNKLTSTALITYIVLTVISLVCGILSLVLACVLMYKOKAQKTLMLWG

540

Db

481

LEENSKLDKVNKLTSTALITYIVLTVIISLVFGILSLILACVLMYKOKAQKTLMLWG

540

Qy

541

NNTLDQMRATTKM

553

Db

541

NNTLDQMRATTKM

553

RESULT 2

US-08-484-575A-14

Sequence 14, Application US/08484575A

Patent No. 5925358

GENERAL INFORMATION:

APPLICANT: Mark D. Cochran and David E. Junker

TITLE OF INVENTION: Recombinant Fowlpox Viruses and Uses Thereof

NUMBER OF SEQUENCES: 42

CORRESPONDENCE ADDRESS:

ADDRESSEE: John P. White

STREET: 1185 Avenue of the Americas

CITY: New York

STATE: New York

COUNTRY: USA

ZIP: 10036

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent In Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/484,575A

FILING DATE: 07-JUN-1995

CLASSIFICATION: 424

ATTORNEY/AGENT INFORMATION:

NAME: White Esq, John P

TELECOMMUNICATION INFORMATION:

TELEPHONE: (212)278-0450

TELEFAX: (212)391-0525

INFORMATION FOR SEQ ID NO: 14:

SEQUENCE CHARACTERISTICS:

LENGTH: 553 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-484-575A-14

TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)977-9550
TELEFAX: (212)664-0525
TELEX: 422523
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 553 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-023-610-13

Query Match 94.7%; Score 2610; DB 2; Length 553;
Best Local Similarity 93.1%; Pred. No. 3.2e-230;
Matches 515; Conservative 21; Mismatches 17; Indels 0; Gaps 0;
QY 1 MGRSSTRIPVPLMLTVRVALALSCVPTSSLDGRPLAAAGIVVTGDKAVNIYTSSTGS 60
DB 1 MGRSPSTKPNPAPMLTIRVALVLSICIPANSIDGRPLAAAGIVVTGDKAVNIYTSSTGS 60
QY 61 IIVKLLPNMPKDEKACAKAPLEAYNRTLTLLPLGDSIRRIQESVTTSGGKQRLIGA 120
DB 61 IIVKLLPNMPKDEKACAKAPLEAYNRTLTLLPLGDSIRRIQESVTTSGGKQRLIGA 120
QY 121 IIGGAALGVATAAQITAAALIQANQNAANILRLKERIAATNEAVHEVTDGLSOLAVAG 180
DB 121 IIGGVALGVATAAQITAAALIQANQNAANILRLKERIAATNEAVHEVTDGLSOLAVAG 180
QY 181 KMQQFVNDQFNKTAQELDCIKITQQVGVNELNLYLTETTTVFGPQITSPALTIQALYN 240
DB 181 KMQQFVNDQFNKTAQELDCIKITQQVGVNELNLYLTETTTVFGPQITSPALTIQALYN 240
QY 241 LAGGNMDYLLTKLGVGNQNLSSLGSLITGNPILYDSQTLGIGIQTLPSPVGNLNNMRA 300
DB 241 LAGGNMDYLLTKLGVGNQNLSSLGSLITGNPILYDSQTLGIGIQTLPSPVGNLNNMRA 300
QY 301 TYLETLSVSTTKGFASALVPKVMKGVSVIEELDTSYCIETDLDLYCTRIIVTPMSPGIY 360
DB 301 TYLETLSVSTTKGFASALVPKVMKGVSVIEELDTSYCIETDLDLYCTRIIVTPMSPGIY 360
QY 361 SCLSGNTSACWYKTEGALTTPYMTLKGSVIANCKMTTCRCADPPGIIISQNYGEAVSLID 420
DB 361 SCLSGNTSACWYKTEGALTTPYMTLKGSVIANCKMTTCRCADPPGIIISQNYGEAVSLID 420
QY 421 ROSCNVLSLDGITRLSGEFDTYQKNISIQDSQVITGNLDISTELGNVNNISNALDK 480
DB 421 KQSCNVLSLGGITRLSGEFDTYQKNISIQDSQVITGNLDISTELGNVNNISNALNK 480
QY 481 LEESSNKLDKVNKLTSTSLALITYIVLTIVLSVCGILSLVACVLMYKQAKQKTLILWL 540
DB 481 LEESSNKLDKVNKLTSTSLALITYIVLTIVLSVCGILSLVACVLMYKQAKQKTLILWL 540
QY 541 NNTLDQMRATTKM 553
DB 541 NNTLDQMRATTKM 553

RESULT 4
US-08-288-065A-13
Sequence 13, Application US/08288065A
Patent No. 5961982
GENERAL INFORMATION:
APPLICANT: Cochran, Mark D
APPLICANT: Macdonald, Richard D
TITLE OF INVENTION: Recombinant Herpesvirus of Turkeys S-
TITLE OF INVENTION: HVT-050 and Uses Thereof
NUMBER OF SEQUENCES: 56
CORRESPONDENCE ADDRESSES:
ADDRESSEE: John P. White
STREET: 1185 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA

ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/288,065A
FILING DATE: Aug-09-94
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: White, John P
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)278-0400
TELEFAX: (212)391-0526
TELEX: 422523
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 553 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-288-065A-13

Query Match 94.7%; Score 2610; DB 2; Length 553;
Best Local Similarity 93.1%; Pred. No. 3.2e-230;
Matches 515; Conservative 21; Mismatches 17; Indels 0; Gaps 0;
QY 1 MGRSSTRIPVPLMLTVRVALALSCVPTSSLDGRPLAAAGIVVTGDKAVNIYTSSTGS 60
DB 1 MGRSPSTKPNPAPMLTIRVALVLSICIPANSIDGRPLAAAGIVVTGDKAVNIYTSSTGS 60
QY 61 IIVKLLPNMPKDEKACAKAPLEAYNRTLTLLPLGDSIRRIQESVTTSGGKQRLIGA 120
DB 61 IIVKLLPNMPKDEKACAKAPLEAYNRTLTLLPLGDSIRRIQESVTTSGGKQRLIGA 120
QY 121 IIGGAALGVATAAQITAAALIQANQNAANILRLKERIAATNEAVHEVTDGLSOLAVAG 180
DB 121 IIGGVALGVATAAQITAAALIQANQNAANILRLKERIAATNEAVHEVTDGLSOLAVAG 180
QY 181 KMQQFVNDQFNKTAQELDCIKITQQVGVNELNLYLTETTTVFGPQITSPALTIQALYN 240
DB 181 KMQQFVNDQFNKTAQELDCIKITQQVGVNELNLYLTETTTVFGPQITSPALTIQALYN 240
QY 241 LAGGNMDYLLTKLGVGNQNLSSLGSLITGNPILYDSQTLGIGIQTLPSPVGNLNNMRA 300
DB 241 LAGGNMDYLLTKLGVGNQNLSSLGSLITGNPILYDSQTLGIGIQTLPSPVGNLNNMRA 300
QY 301 TYLETLSVSTTKGFASALVPKVMKGVSVIEELDTSYCIETDLDLYCTRIIVTPMSPGIY 360
DB 301 TYLETLSVSTTKGFASALVPKVMKGVSVIEELDTSYCIETDLDLYCTRIIVTPMSPGIY 360
QY 361 SCLSGNTSACWYKTEGALTTPYMTLKGSVIANCKMTTCRCADPPGIIISQNYGEAVSLID 420
DB 361 SCLSGNTSACWYKTEGALTTPYMTLKGSVIANCKMTTCRCADPPGIIISQNYGEAVSLID 420
QY 421 ROSCNVLSLDGITRLSGEFDTYQKNISIQDSQVITGNLDISTELGNVNNISNALDK 480
DB 421 KQSCNVLSLGGITRLSGEFDTYQKNISIQDSQVITGNLDISTELGNVNNISNALNK 480
QY 481 LEESSNKLDKVNKLTSTSLALITYIVLTIVLSVCGILSLVACVLMYKQAKQKTLILWL 540
DB 481 LEESSNKLDKVNKLTSTSLALITYIVLTIVLSVCGILSLVACVLMYKQAKQKTLILWL 540
QY 541 NNTLDQMRATTKM 553
DB 541 NNTLDQMRATTKM 553

RESULT 5
US-08-362-240A-13
Sequence 13, Application US/08362240A
Patent No. 5965138

```

GENERAL INFORMATION:
APPLICANT: Cochran, Mark D
APPLICANT: Junker, David
APPLICANT: Wild, Martha A
TITLE OF INVENTION: Recombinant Herpesvirus and Uses Thereof
NUMBER OF SEQUENCES: 60
CORRESPONDENCE ADDRESS:
ADDRESSEE: John P. White
STREET: 1185 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/362,240A
FILING DATE: Dec-22-94
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: White, John P
REGISTRATION NUMBER: 28,678
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)278-0400
TELEFAX: (212)391-0526
TELEX: 422523
INFORMATION FOR SEQ ID NO: 13:
LENGTH: 553 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-362-240A-13

Query Match          94.7%; Score 2610; DB 2; Length 553;
Best Local Similarity 93.1%; Pred. No. 3.2e-230;
Matches 515; Conservative 21; Mismatches 17; Indels 0; Gaps 0;

Qy 1 MGRSSTRIPVPLMLTVRVALSCVPTSSLDGRPLAAAGIVVTGDKAVNIYTSQTGS 60
Db 1 MGRSPSTKNPAPMLTIRVALVSLCIPANSIDGRPLAAAGIVVTGDKAVNIYTSQTGS 60
Qy 61 IIVKLLPNMPKDKKACAKAPLEAYNRTLTLLTPLGDSIRRIQESVTTSGGKQGRLLGA 120
Db 61 IIVKLLPNLPKDKKACAKAPLDAYNRTLTLLTPLGDSIRRIQESVTTSGGKQGRLLGA 120
Qy 121 IIGGAALGVATAAQITAAALIOAQNAAIIRLKERIAATNEAVHEVTDGLSQLAVAG 180
Db 121 IIGGVALGVATAAQITAAALIOAQNAAIIRLKERIAATNEAVHEVTDGLSQLAVAG 180
Qy 181 KMQQFVNDQFNKTAQELDCIKITQQGVVELNLYLTETLTVFGPQITSPALTLTIQALYN 240
Db 181 KMQQFVNDQFNKTAQELDCIKITQQGVVELNLYLTETLTVFGPQITSPALTLTIQALYN 240
Qy 241 LAGGNMDDLKLGVNNQLSSLGSLITGNPILYDSQTQLLGIQVTLPSVGNLNNMRA 300
Db 241 LAGGNMDDLKLGIGNNQLSSLGSLITGNPILYDSQTQLLGIQVTLPSVGNLNNMRA 300
Qy 301 TYLETLSVSTTKGFASALVPKVMKGVSVIEELDTSCYIETDLDLYCTRIVTFPMSPGIY 360
Db 301 TYLETLSVSTTKGFASALVPKVMKGVSVIEELDTSCYIETDLDLYCTRIVTFPMSPGIY 360
Qy 361 SCLSGNTSACMYSKTEGALTTPYMTLKGSVIANCKMTTCRCADPPGIIISQNYGEAVSLID 420
Db 361 SCLSGNTSACMYSKTEGALTTPYMTLKGSVIANCKMTTCRCVNPPIIISQNYGEAVSLID 420
Qy 421 ROSCNVLSIDGTTLRSGEFDATYOKNISIDQSVIVTCNLIDISTELGNVNNISNALDK 480
Db 421 KQSCNVLSLGGITLRSGEFDVYOKNISIQDSVIITGNLIDISTELGNVNNISNALNK 480

GENERAL INFORMATION:
APPLICANT: Cochran, Mark D
APPLICANT: Junker, David
APPLICANT: Wild, Martha A
TITLE OF INVENTION: Recombinant Herpesvirus and Uses Thereof
NUMBER OF SEQUENCES: 60
CORRESPONDENCE ADDRESS:
ADDRESSEE: John P. White
STREET: 1185 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/477,459
FILING DATE: 07-JUN-1995
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: White Esq, John P
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 278-0400
TELEFAX: (212) 391-0525
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 553 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-477-459-14

Query Match          94.7%; Score 2610; DB 3; Length 553;
Best Local Similarity 93.1%; Pred. No. 3.2e-230;
Matches 515; Conservative 21; Mismatches 17; Indels 0; Gaps 0;

Qy 1 MGRSSTRIPVPLMLTVRVALSCVPTSSLDGRPLAAAGIVVTGDKAVNIYTSQTGS 60
Db 1 MGRSPSTKNPAPMLTIRVALVSLCIPANSIDGRPLAAAGIVVTGDKAVNIYTSQTGS 60
Qy 61 IIVKLLPNMPKDKKACAKAPLEAYNRTLTLLTPLGDSIRRIQESVTTSGGKQGRLLGA 120
Db 61 IIVKLLPNLPKDKKACAKAPLDAYNRTLTLLTPLGDSIRRIQESVTTSGGKQGRLLGA 120
Qy 121 IIGGAALGVATAAQITAAALIOAQNAAIIRLKERIAATNEAVHEVTDGLSQLAVAG 180
Db 121 IIGGVALGVATAAQITAAALIOAQNAAIIRLKERIAATNEAVHEVTDGLSQLAVAG 180
Qy 181 KMQQFVNDQFNKTAQELDCIKITQQGVVELNLYLTETLTVFGPQITSPALTLTIQALYN 240
Db 181 KMQQFVNDQFNKTAQELDCIKITQQGVVELNLYLTETLTVFGPQITSPALTLTIQALYN 240
Qy 241 LAGGNMDDLKLGVNNQLSSLGSLITGNPILYDSQTQLLGIQVTLPSVGNLNNMRA 300
Db 241 LAGGNMDDLKLGIGNNQLSSLGSLITGNPILYDSQTQLLGIQVTLPSVGNLNNMRA 300
Qy 301 TYLETLSVSTTKGFASALVPKVMKGVSVIEELDTSCYIETDLDLYCTRIVTFPMSPGIY 360
Db 301 TYLETLSVSTTKGFASALVPKVMKGVSVIEELDTSCYIETDLDLYCTRIVTFPMSPGIY 360
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Db 301 TYLETSLVSTTRGFASALVPKVVTRVGVSVIEELDTSYCIETDLDLYCTRIVTFPMSPGIY 360
QY 361 SCLSGNTSACWYKTEGALTTPYMTLKGSVIANCKMTTCRCADPPGIISQNYGEAVSLID 420
Db 361 SCLSGNTSACWYKTEGALTTPYMTLKGSVIANCKMTTCRCVNPPIISQNYGEAVSLID 420
QY 421 RQSCNVLSLGDITLRLSGEFDATYQKNISIQDSQVIVTGNLDISTELGNVNSISNALDK 480
Db 421 RQSCNVLSLGDITLRLSGEFDATYQKNISIQDSQVIVTGNLDISTELGNVNSISNALDK 480
QY 481 LEESNSKLDKVNKLTSTLSALITYIVLTIVSLVCGILSLVLACVLMYKQKQAOKTLLWL 540
Db 481 LEESNRKLDKVNKLTSTLSALITYIVLTIVSLVCGILSLVLACVLMYKQKQAOKTLLWL 540
QY 541 NNTLDQMRATTKM 553
Db 541 NNTLDQMRATTKM 553

RESULT 7

US-08-479-869-14
; Sequence 14, Application US/08479869
; Patent No. 6123949
; GENERAL INFORMATION:
; APPLICANT: Cochran Ph.D, Mark D
; TITLE OF INVENTION: Recombinant Fowlpox Virus S-FPV-043 and
; TITLE OF INVENTION: Uses Thereof
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: John P. White
; STREET: 30 Rockefeller Plaza
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10112
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/479,869
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/024,156
; FILING DATE: 26-FEB-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: White Esq, John P
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212)977-9550
; TELEFAX: (212)664-0525
; TELEX: 422523
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 553 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-479-869-14

Query Match 94.7%; Score 2610; DB 3; Length 553;
Best Local Similarity 93.1%; Pred. No. 3.2e-230;
Matches 515; Conservative 21; Mismatches 17; Indels 0; Gaps 0;
QY 1 MGRSSTRIPVPLMLTVRVALALSCVCPSSLDGRPLAAAGIVVTGDKAVNIYTSOTGS 60
Db 1 MGRSPSTKPNPWWLTIRVALVLSLSCIPANSIDGRPLAAAGIVVTGDKAVNIYTSOTGS 60
QY 61 IIVKLLPNPKDKEACAKAPLEAYNRTLTLLTLPGLDSIRRIQESVTTSGGKQGRLLIGA 120
Db 61 IIVKLLPNPKDKEACAKAPLEAYNRTLTLLTLPGLDSIRRIQESVTTSGGKQGRLLIGA 120

QY 121 IIGGAALGVATAAQITAAASALIQANQANANILRLKERIAATNEAVHEVTDGLSOLAVAG 180
Db 121 IIGGAALGVATAAQITAAASALIQANQANANILRLKERIAATNEAVHEVTDGLSOLAVAG 180
QY 181 KMQQFVNDQFNKTAQELDCIKITQQGVGVELNLVLTETTVFGPQITSPALTIQALYN 240
Db 181 KMQQFVNDQFNKTAQELDCIKITQQGVGVELNLVLTETTVFGPQITSPALTIQALYN 240
QY 241 LAGNMDYLLTKLGVGNQNLSSLIGSLITGNPILYDSQTLGLIQVTLFSPVGNLNMRA 300
Db 241 LAGNMDYLLTKLGVGNQNLSSLIGSLITGNPILYDSQTLGLIQVTLFSPVGNLNMRA 300
QY 301 TYLETSLVSTTRGFASALVPKVVTRVGVSVIEELDTSYCIETDLDLYCTRIVTFPMSPGIY 360
Db 301 TYLETSLVSTTRGFASALVPKVVTRVGVSVIEELDTSYCIETDLDLYCTRIVTFPMSPGIY 360
QY 361 SCLSGNTSACWYKTEGALTTPYMTLKGSVIANCKMTTCRCADPPGIISQNYGEAVSLID 420
Db 361 SCLSGNTSACWYKTEGALTTPYMTLKGSVIANCKMTTCRCVNPPIISQNYGEAVSLID 420
QY 421 RQSCNVLSLGDITLRLSGEFDATYQKNISIQDSQVIVTGNLDISTELGNVNSISNALDK 480
Db 421 RQSCNVLSLGDITLRLSGEFDATYQKNISIQDSQVIVTGNLDISTELGNVNSISNALDK 480
QY 481 LEESNSKLDKVNKLTSTLSALITYIVLTIVSLVCGILSLVLACVLMYKQKQAOKTLLWL 540
Db 481 LEESNRKLDKVNKLTSTLSALITYIVLTIVSLVCGILSLVLACVLMYKQKQAOKTLLWL 540
QY 541 NNTLDQMRATTKM 553
Db 541 NNTLDQMRATTKM 553

RESULT 8

US-08-486-414-14
; Sequence 14, Application US/08486414B
; Patent No. 613318
; GENERAL INFORMATION:
; APPLICANT: Cochran, Mark D.
; APPLICANT: Junker, David E.
; TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUSES AND USES THEREOF
; FILE REFERENCE: 4277LD
; CURRENT APPLICATION NUMBER: US/08/486,414B
; CURRENT FILING DATE: 1995-06-07
; NUMBER OF SEQ ID NOS: 46
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 14
; LENGTH: 553
; TYPE: PRT
; ORGANISM: Fowlpox virus
US-08-486-414-14

Query Match 94.7%; Score 2610; DB 3; Length 553;
Best Local Similarity 93.1%; Pred. No. 3.2e-230;
Matches 515; Conservative 21; Mismatches 17; Indels 0; Gaps 0;

QY 1 MGRSSTRIPVPLMLTVRVALALSCVCPSSLDGRPLAAAGIVVTGDKAVNIYTSOTGS 60
Db 1 MGRSPSTKPNPWWLTIRVALVLSLSCIPANSIDGRPLAAAGIVVTGDKAVNIYTSOTGS 60
QY 61 IIVKLLPNPKDKEACAKAPLEAYNRTLTLLTLPGLDSIRRIQESVTTSGGKQGRLLIGA 120
Db 61 IIVKLLPNPKDKEACAKAPLEAYNRTLTLLTLPGLDSIRRIQESVTTSGGKQGRLLIGA 120
QY 121 IIGGAALGVATAAQITAAASALIQANQANANILRLKERIAATNEAVHEVTDGLSOLAVAG 180
Db 121 IIGGAALGVATAAQITAAASALIQANQANANILRLKERIAATNEAVHEVTDGLSOLAVAG 180
QY 181 KMQQFVNDQFNKTAQELDCIKITQQGVGVELNLVLTETTVFGPQITSPALTIQALYN 240
Db 181 KMQQFVNDQFNKTAQELDCIKITQQGVGVELNLVLTETTVFGPQITSPALTIQALYN 240
QY 241 LAGNMDYLLTKLGVGNQNLSSLIGSLITGNPILYDSQTLGLIQVTLFSPVGNLNMRA 300

Db 241 LAGNMDVLLKLGIGNNQSSLGSLITGNPILYDSOTQLGLQVTLPSVGNLNNRA 300
QY 301 TYLETSLVSTTKGFASALVPKVMKGVSVIEBELDTSYCIETDLDLYCTRIVTFPMSPGIY 360
Db 301 TYLETSLVSTTKGFASALVPKVMKGVSVIEBELDTSYCIETDLDLYCTRIVTFPMSPGIY 360
QY 361 SCLSGNTSACMYSKTEGALTTPYMTIKGVSIVANCKMTTCRCADPPGIIISQNYGEAVSLID 420
Db 361 SCLSGNTSACMYSKTEGALTTPYMTIKGVSIVANCKMTTCRCVNPPIISQNYGEAVSLID 420
QY 421 RQSCNVLSLGGITLRLSGEFDATYQKNISIQDSQVIVTGNLIDISTELGNVNNISNALDK 480
Db 421 RQSCNVLSLGGITLRLSGEFDVYQKNISIQDSQVIVTGNLIDISTELGNVNNISNALNK 480
QY 481 LEESNKLDKVNKLTSTTSALITYIVLVISVCGILSLVACVIMYKQKQKQKLLMWG 540
Db 481 LEESNKLDKVNKLTSTTSALITYIVLVISVCGILSLVACVIMYKQKQKQKLLMWG 540
QY 541 NNTLDMRATTM 553
Db 541 NNTLDMRATTM 553

RESULT 9

US-08-804-372A-11
; Sequence 11, Application US/08804372A
; Patent No. 6183753
; GENERAL INFORMATION:
; APPLICANT: Cochran, Mark D.
; APPLICANT: Wild, Martha A.
; APPLICANT: Winslow, Barbara J.
; TITLE OF INVENTION: Recombinant Chimeric Viruses and Uses
; TITLE OF INVENTION: Thereof
; NUMBER OF SEQUENCES: 32
; CORRESPONDENCE ADDRESS:
; STREET: 1185 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; FILING DATE:
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: White, John P.
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 2552/39115E
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 278-0400
; TELEFAX: (212) 391-0525
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 553 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein

US-08-804-372A-11
Query Match 94.7%; Score 2610; DB 3; Length 553;
Best Local Similarity 93.1%; Pred. No. 3.2e-230;
Matches 515; Conservative 21; Mismatches 17; Indels 0; Gaps 0;

QY 1 MGSRSSTRPVLMLTVRVALSCVCPSTSSLDGRPLAAGIVVTGDKAVNIYTSQTGS 60
Db 1 MGSRSSTRPVLMLTVRVALSCVCPSTSSLDGRPLAAGIVVTGDKAVNIYTSQTGS 60

QY 61 IIVKLLPNMPKDKKACAPLEAYNRTLTLLTLPDGSIRRIQESVTTSGGKQGRLLGA 120
Db 61 IIVKLLPNLPKDKKACAPLADAYNRTLTLLTLPDGSIRRIQESVTTSGGKQGRLLGA 120
QY 121 IIGGAALGVATAAQITAAASALIQANQNAANTLRKERIAATNEAVHEVTDGLSQLAVAVG 180
Db 121 IIGGVALGVATAAQITAAALIQAKNAANILRLKESIAATNEAVHEVTDGLSQLAVAVG 180
QY 181 KMOQFVNDQFNKTAQELDCIKITQOVGVVELNLYLTETTFVGPQITSPALQITQALYN 240
Db 181 KMOQFVNDQFNKTAQELDCIKIAQOVGVVELNLYLTETTFVGPQITSPALNKLITQALYN 240
QY 241 LAGNMDVLLKLGIGNNQSSLGSLITGNPILYDSOTQLGLQVTLPSVGNLNNRA 300
Db 241 LAGNMDVLLKLGIGNNQSSLGSLITGNPILYDSOTQLGLQVTLPSVGNLNNRA 300
QY 301 TYLETSLVSTTKGFASALVPKVMKGVSVIEBELDTSYCIETDLDLYCTRIVTFPMSPGIY 360
Db 301 TYLETSLVSTTKGFASALVPKVMKGVSVIEBELDTSYCIETDLDLYCTRIVTFPMSPGIY 360
QY 361 SCLSGNTSACMYSKTEGALTTPYMTIKGVSIVANCKMTTCRCADPPGIIISQNYGEAVSLID 420
Db 361 SCLSGNTSACMYSKTEGALTTPYMTIKGVSIVANCKMTTCRCVNPPIISQNYGEAVSLID 420
QY 421 RQSCNVLSLGGITLRLSGEFDATYQKNISIQDSQVIVTGNLIDISTELGNVNNISNALDK 480
Db 421 RQSCNVLSLGGITLRLSGEFDVYQKNISIQDSQVIVTGNLIDISTELGNVNNISNALNK 480
QY 481 LEESNKLDKVNKLTSTTSALITYIVLVISVCGILSLVACVIMYKQKQKQKLLMWG 540
Db 481 LEESNKLDKVNKLTSTTSALITYIVLVISVCGILSLVACVIMYKQKQKQKLLMWG 540
QY 541 NNTLDMRATTM 553
Db 541 NNTLDMRATTM 553

RESULT 10
PCT-US94-01826A-14
; Sequence 14, Application PC/TUS9401826A
; GENERAL INFORMATION:
; APPLICANT: Syntro Corporation, et al.
; TITLE OF INVENTION: Recombinant Fowlpox Virus S-FPV-043 and Uses Thereof
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: John P. White
; STREET: 30 Rockefeller Plaza
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10112
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/01826A
; FILING DATE: 28-FEB-1994
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: White Esq, John P
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 977-9550
; TELEFAX: (212) 664-0525
; TELEX: 422523
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 553 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein

PCT-US94-01826A-14

Query Match 94.7%; Score 2610; DB 5; Length 553;
Best Local Similarity 93.1%; Pred. No. 3.2e-230;
Matches 515; Conservative 21; Mismatches 17; Indels 0; Gaps 0;

QY 1 MGRSSSTRIPVPLMLTVRVALALSCVPTSSLDGRPLAAAGIVVTGDKAVNIYTSSQTGS 60
DB 1 MGRSPSTKNPAPMLTIRVALVLSICIPANSIDGRPLAAAGIVVTGDKAVNIYTSSQTGS 60

QY 61 IIVKLLPNMPKDEACAKAPLEAYNRTLTLLTLPGLDSIRRIQESVITSSGGKQGRLLGA 120
DB 61 IIVKLLPNLPKDEACAKAPLEAYNRTLTLLTLPGLDSIRRIQESVITSSGGKQGRLLGA 120

QY 121 IIGGAALGVATAAQITAAASALIQANQANALIRLKERIAATNEAVHEVTDGLSOLAVAVG 180
DB 121 IIGGVALGVATAAQITAAASALIQANQANALIRLKERIAATNEAVHEVTDGLSOLAVAVG 180

QY 181 KMQQFVNDQFNKTAQELDCIKITQOVGVNELNLYLTETTVFGPOITSPALTLTQIALYN 240
DB 181 KMQQFVNDQFNKTAQELDCIKITQOVGVNELNLYLTETTVFGPOITSPALTLTQIALYN 240

QY 241 LAGNMDYLLTKLGVGNQNLSSGLITGNPILYDSQTQLLGIQVTLPSVGNLNNMRA 300
DB 241 LAGNMDYLLTKLGVGNQNLSSGLITGNPILYDSQTQLLGIQVTLPSVGNLNNMRA 300

QY 301 TYLETLSVSTTKGFASALVPKVMKGVSVIEELDTSYCIETDLDLYCTRIIVTFPMSPGIY 360
DB 301 TYLETLSVSTTRGFASALVPKVMKGVSVIEELDTSYCIETDLDLYCTRIIVTFPMSPGIY 360

QY 361 SCLSGNTSACMYSKTEGALTTPYMTLKGSVIANCKMTTCRCADPPGIISQNYGEAVSLID 420
DB 361 SCLSGNTSACMYSKTEGALTTPYMTLKGSVIANCKMTTCRCVNPFGIISQNYGEAVSLID 420

QY 421 RQSCNVLSLGDITLRLSGEFDATYQKNISIQDSQVIVTGNLIDISTELGNVNNISNALDK 480
DB 421 RQSCNVLSLGGITLRLSGEFDVTVYQKNISIQDSQVITGNLIDISTELGNVNNISNALNK 480

QY 481 LEESNKLKDVNKLSTSLITYVILTVISLVCGLISLVLACVLYMKQKAAQKTLWLWG 540
DB 481 LEESNRKLDKVNKLSTSLITYVILTVISLVCGLISLVLACVLYMKQKAAQKTLWLWG 540

QY 541 NNTLDQMRATTKM 553
DB 541 NNTLDQMRATTKM 553

RESULT 11

PCT-US94-02252A-14
Sequence 14, Application PC/TUS9402252A
GENERAL INFORMATION:
APPLICANT: Synro Corporation, et al.
TITLE OF INVENTION: Recombinant Fowlpox Viruses and Uses Thereof
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
ADDRESSEE: John P. White
STREET: 30 Rockefeller Plaza
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10112
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/02252A
FILING DATE: 28-FEB-1994
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: White Esq. John P
TELECOMMUNICATION INFORMATION:

TELEPHONE: (212)977-9550
TELEFAX: (212)664-0525
TELEX: 422523
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 553 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
PCT-US94-02252A-14

Query Match 94.7%; Score 2610; DB 5; Length 553;
Best Local Similarity 93.1%; Pred. No. 3.2e-230;
Matches 515; Conservative 21; Mismatches 17; Indels 0; Gaps 0;

QY 1 MGRSSSTRIPVPLMLTVRVALALSCVPTSSLDGRPLAAAGIVVTGDKAVNIYTSSQTGS 60
DB 1 MGRSPSTKNPAPMLTIRVALVLSICIPANSIDGRPLAAAGIVVTGDKAVNIYTSSQTGS 60

QY 61 IIVKLLPNMPKDEACAKAPLEAYNRTLTLLTLPGLDSIRRIQESVITSSGGKQGRLLGA 120
DB 61 IIVKLLPNLPKDEACAKAPLEAYNRTLTLLTLPGLDSIRRIQESVITSSGGKQGRLLGA 120

QY 121 IIGGAALGVATAAQITAAASALIQANQANALIRLKERIAATNEAVHEVTDGLSOLAVAVG 180
DB 121 IIGGVALGVATAAQITAAASALIQANQANALIRLKERIAATNEAVHEVTDGLSOLAVAVG 180

QY 181 KMQQFVNDQFNKTAQELDCIKITQOVGVNELNLYLTETTVFGPOITSPALTLTQIALYN 240
DB 181 KMQQFVNDQFNKTAQELDCIKITQOVGVNELNLYLTETTVFGPOITSPALTLTQIALYN 240

QY 241 LAGNMDYLLTKLGVGNQNLSSGLITGNPILYDSQTQLLGIQVTLPSVGNLNNMRA 300
DB 241 LAGNMDYLLTKLGVGNQNLSSGLITGNPILYDSQTQLLGIQVTLPSVGNLNNMRA 300

QY 301 TYLETLSVSTTKGFASALVPKVMKGVSVIEELDTSYCIETDLDLYCTRIIVTFPMSPGIY 360
DB 301 TYLETLSVSTTRGFASALVPKVMKGVSVIEELDTSYCIETDLDLYCTRIIVTFPMSPGIY 360

QY 361 SCLSGNTSACMYSKTEGALTTPYMTLKGSVIANCKMTTCRCADPPGIISQNYGEAVSLID 420
DB 361 SCLSGNTSACMYSKTEGALTTPYMTLKGSVIANCKMTTCRCVNPFGIISQNYGEAVSLID 420

QY 421 RQSCNVLSLGDITLRLSGEFDATYQKNISIQDSQVIVTGNLIDISTELGNVNNISNALDK 480
DB 421 RQSCNVLSLGGITLRLSGEFDVTVYQKNISIQDSQVITGNLIDISTELGNVNNISNALNK 480

QY 481 LEESNKLKDVNKLSTSLITYVILTVISLVCGLISLVLACVLYMKQKAAQKTLWLWG 540
DB 481 LEESNRKLDKVNKLSTSLITYVILTVISLVCGLISLVLACVLYMKQKAAQKTLWLWG 540

QY 541 NNTLDQMRATTKM 553
DB 541 NNTLDQMRATTKM 553

RESULT 12

PCT-US95-10245-13
Sequence 13, Application PC/TUS9510245
GENERAL INFORMATION:
APPLICANT: SYNRO CORPORATION
TITLE OF INVENTION: Recombinant Herpesvirus of Turkeys And Uses Thereof
NUMBER OF SEQUENCES: 60
CORRESPONDENCE ADDRESS:
ADDRESSEE: John P. White
STREET: 1185 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/10245
FILING DATE: 09-AUG-1995
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: White, John P
REGISTRATION NUMBER: 28,678
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)278-0400
TELEFAX: (212)391-0526
TELEX: 422523
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 553 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
PCT-US95-10245-13

Query Match 94.7%; Score 2610; DB 5; Length 553;
Best Local Similarity 93.1%; Pred. No. 3.2e-230;
Matches 515; Conservative 21; Mismatches 17; Indels 0; Gaps 0;
QY 1 MGRSSSTRIIPVPLMLTVRVALALSCVPTSSLDGRPLAAAGIVVTGDKAVNIYTSSTQGS 60
DB 1 MGRPSTKNPAPMLTIIRVALVLSICIPANSIDGRPLAAAGIVVTGDKAVNIYTSSTQGS 60
QY 61 IIVKLLPNMPKDKKACAKAPLEAYNRTLTLLTPLGDSIRRIQESVTTSGGKQRLIGA 120
DB 61 IIVKLLPNLPKDKKACAKAPLDAYNRTLTLLTPLGDSIRRIQESVTTSGGKQRLIGA 120
QY 121 IIGGAALGVATAAQTAAALIQANQNAANILRLKERTAAEAHVETDGLSQLAVAG 180
DB 121 IIGGVALGVATAAQTAAALIQANQNAANILRLKESIAATNEAHEVETDGLSQLAVAG 180
QY 181 KMQQFVNDQFNKTAQELDCIKITQOVGVLELNLXLTETTVFGPQITSPALTOITQALYN 240
DB 181 KMQQFVNDQFNKTAQELDCIKIAQOVGVLELNLXLTETTVFGPQITSPALNKLTITQALYN 240
QY 241 LAGNMNDYLLTKLGVGNQNLSSLGSLITGNPILYDSQTLGLGIVTLPSVGNLNNMRA 300
DB 241 LAGNMNDYLLTKLGVGNQNLSSLGSLITGNPILYDSQTLGLGIVTLPSVGNLNNMRA 300
QY 301 TYLETSLVSTTKGFASALVPKVMKGVSVIEELDTSYCIETDLDLYCTRIVTFPMSPGIY 360
DB 301 TYLETSLVSTTRGFASALVPKVMKGVSVIEELDTSYCIETDLDLYCTRIVTFPMSPGIY 360
QY 361 SCLSGNTSACMYSKTEGALTTPYMTLKGSVIANCKMTTCRCADPPGIISQNYGEAVSLID 420
DB 361 SCLSGNTSACMYSKTEGALTTPYMTLKGSVIANCKMTTCRCVNPFGIISQNYGEAVSLID 420
QY 421 PQSCNVLSLDGITLRLSGEFDATYQKNISIQDSQVIVTGNLIDISTELGNVNNISNALDK 480
DB 421 PQSCNVLSLDGITLRLSGEFDATYQKNISIQDSQVIVTGNLIDISTELGNVNNISNALNK 480
QY 481 LEESNSKLDKVNKLTSTALITYIVLTIVISLVCGLISLVACILMYKQKQKQKTLMLG 540
DB 481 LEESNRKLDKVNKLTSTALITYIVLTIVLTIIISLVFGILSLVACILMYKQKQKQKTLMLG 540
QY 541 NNTLDQMRATTKM 553
DB 541 NNTLDQMRATTKM 553

RESULT 13

5310678-1
Patent No. 5310678
Applicant: Bingham, Richard W.; Chambers, Philip; Emmerson, Peter
T.; Millar, Neil S.
Title of Invention: NEWCASTLE DISEASE VIRUS GENE CLONES
Number of Sequences: 3

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/438,945
FILING DATE: 17-NOV-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 885,765
FILING DATE: 15-JUL-1986
SEQ ID NO: 1:
LENGTH: 553
5310678-1

Query Match 93.3%; Score 2572; DB 6; Length 553;
Best Local Similarity 92.8%; Pred. No. 9.8e-227;
Matches 513; Conservative 20; Mismatches 20; Indels 0; Gaps 0;
QY 1 MGRSSSTRIIPVPLMLTVRVALALSCVPTSSLDGRPLAAAGIVVTGDKAVNIYTSSTQGS 60
DB 1 MGRPSTKNPVPVPMMLTVRVALVLSICIPANSIDGRPLAAAGIVVTGDKAVNIYTSSTQGS 60
QY 61 IIVKLLPNMPKDKKACAKAPLEAYNRTLTLLTPLGDSIRRIQESVTTSGGKQRLIGA 120
DB 61 IIVKLLPNLPKDKKACAKAPLDAYNRTLTLLTPLGDSIRRIQESVTTSGGKQRLIGA 120
QY 121 IIGGAALGVATAAQTAAALIQANQNAANILRLKERTAAEAHVETDGLSQLAVAG 180
DB 121 IIGGVALGVATAAQTAAALIQANQNAANILRLKESIAATNEAHEVETDGLSQLAVAG 180
QY 181 KMQQFVNDQFNKTAQELDCIKITQOVGVLELNLXLTETTVFGPQITSPALTOITQALYN 240
DB 181 KMQQFVNDQFNKTAQELDCIKIAQOVGVLELNLXLTETTVFGPQITSPALNKLTITQALYN 240
QY 241 LAGNMNDYLLTKLGVGNQNLSSLGSLITGNPILYDSQTLGLGIVTLPSVGNLNNMRA 300
DB 241 LAGNMNDYLLTKLGVGNQNLSSLGSLITGNPILYDSQTLGLGIVTLPSVGNLNNMRA 300
QY 301 TYLETSLVSTTKGFASALVPKVMKGVSVIEELDTSYCIETDLDLYCTRIVTFPMSPGIY 360
DB 301 TYLETSLVSTTRGFASALVPKVMKGVSVIEELDTSYCIETDLDLYCTRIVTFPMSPGIY 360
QY 361 SCLSGNTSACMYSKTEGALTTPYMTLKGSVIANCKMTTCRCADPPGIISQNYGEAVSLID 420
DB 361 SCLSGNTSACMYSKTEGALTTPYMTLKGSVIANCKMTTCRCVNPFGIISQNYGEAVSLID 420
QY 421 PQSCNVLSLDGITLRLSGEFDATYQKNISIQDSQVIVTGNLIDISTELGNVNNISNALDK 480
DB 421 PQSCNVLSLDGITLRLSGEFDATYQKNISIQDSQVIVTGNLIDISTELGNVNNISNALNK 480
QY 481 LEESNSKLDKVNKLTSTALITYIVLTIVISLVCGLISLVACILMYKQKQKQKTLMLG 540
DB 481 LEESNSKLDKVNKLTSTALITYIVLTIVLTIIISLVFGILSLVACILMYKQKQKQKTLMLG 540
QY 541 NNTLDQMRATTKM 553
DB 541 NNTLDQMRATTKM 553

RESULT 14

US-08-486-099-94
Sequence 94, Application US/08486099
Patent No. 6013263
GENERAL INFORMATION:
APPLICANT: Bolognesi, Dani P.
APPLICANT: Matthews, Thomas J.
APPLICANT: Wild, Carl T.
APPLICANT: Barney, Shawn O.
APPLICANT: Lambert, Dennis M.
APPLICANT: Petteway, Stephen R.
APPLICANT: Langlois, Alphonse J.
TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF
MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING HEPATITIS
B VIRUS TRANSMISSION
NUMBER OF SEQUENCES: 209
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds

```
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/486,099
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A.
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 7872-031
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 94:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 436 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; US-08-486-099-94

Query Match 75.7%; Score 2086.5; DB 3; Length 436;
Best Local Similarity 96.6%; Pred. No. 1.9e-182;
Matches 421; Conservative 2; Mismatches 12; Indels 1; Gaps 1;

QY 118 IGAIIGGAALGVATAAQITAAASALIQANQNAANILRLKERIAATNEAVHEVTDGLSOLAV 177
Db 2 IGAIIGSVLGVATAAQITAAASALIQANQNAANILRLKESITATIEAVHEVTDGLSOLAV 61
QY 178 AVGKMQQFVNDQFNKTAQELDCIKITQOVGVNELNLYLTETLVFGPOITSPALTLTQIA 237
Db 62 AVGKMQQFVNDQFNNTAQELDCIKITQOVGVNELNLYLTETLVFGPOITSPALTLTQIA 121
QY 238 LYNLAGNMDYLLTKLGVGNQNSLLIGSLITGNPILYDSQTLGLIQVTLPSVGNLNN 297
Db 122 LYN-AGNMDYLLTKLGVGNQNSLLIGSLITGNPILYDSQTLGLIQVTLPSVGNLNN 180
QY 298 MRATYLETLVSSTTKGFASALVPKVMKGVSVIEELDTSYCIETDLDLYCTRIVTFFMSP 357
Db 181 MRATYLETLVSSTTKGFASALVPKVMKGVSVIEELDTSYCIETDLDLYCTRIVTFFMSP 240
QY 358 GIYSCLSGNTSACMYSKTEGALTTPYMTLKGSVIANCKMTTCRCADPPGIISQNYGEAVS 417
Db 241 GIYSCLSGNTSACMYSKTEGALTTPYMTLKGSVIANCKMTTCRCADPPGIISQNYGEAVS 300
QY 418 LIDRQSCNVLSLDGITLRLSGEFDATYQKNISIQDSQVIVTGNLDISTELGNVNNISNA 477
Db 301 LIDRHSCNVLSLDGITLRLSGEFDATYQKNISILDSQVIVTGNLDISTELGNVNNISNA 360
QY 478 LDKLEESNSKLDKVNKLTSTALITYIVLTIVSLVCGILSLVACLYMYKQKQAKTLL 537
Db 361 LDKLEESNSKLDKVNKLTSTALITYIVLTIVSLVCGILSLVACLYMYKQKQAKTLL 420
QY 538 WLGNNTLDQMRATTKM 553
Db 421 WLGNNTLDQMRATTKM 436

RESULT 15
US-08-360-107A-104
; Sequence 104, Application US/08360107A
; Patent No. 6017536
; GENERAL INFORMATION:
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Db 361 LDKLEESNSKLDKVNKLTSTISALITYTALTATISLVCGILSVLACHLMYKQKQKTL 420
Qy 538 WLGNTLQMRATTKM 553
Db 421 WLGNTLQMRATTKM 436

Search completed: April 18, 2004, 02:34:36
Job time : 52 secs

GenCore version 5.1.6
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QM protein - protein search, using sw model

Run on: April 18, 2004, 01:23:45 ; Search time 81 Seconds
(without alignments)
1882.065 Million cell updates/sec

Title: US-10-725-841-2

Perfect score: 2757

Sequence: 1 MGRSRSTRPVPPLMLTVRVA.....XTLLWLGNTLDQMRATYTM 553

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1124875 seqs, 275673149 residues

Total number of hits satisfying chosen parameters: 1124875

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2493.5	90.4	564	9 US-09-881-457A-2	Sequence 2, Appli
2	2086.5	75.7	436	12 US-10-267-682-94	Sequence 94, Appl
3	2086.5	75.7	436	12 US-10-267-748-94	Sequence 94, Appl
4	623.5	22.6	662	10 US-09-951-061A-141	Sequence 141, App
5	621.5	22.5	662	12 US-10-670-695-36	Sequence 36, Appl
6	606.5	22.0	550	9 US-09-873-233A-20	Sequence 18, Appl
7	605.5	22.0	550	9 US-09-873-233A-18	Sequence 18, Appl
8	534	19.4	438	12 US-10-267-682-93	Sequence 93, Appl
9	534	19.4	438	12 US-10-267-748-93	Sequence 93, Appl
10	504	18.3	438	12 US-10-267-682-105	Sequence 105, App
11	504	18.3	438	12 US-10-267-748-105	Sequence 105, App
12	458	16.6	430	12 US-10-267-682-95	Sequence 95, Appl
13	458	16.6	430	12 US-10-267-748-95	Sequence 95, Appl
14	211	7.7	574	15 US-10-371-264-6	Sequence 6, Appli
15	211	7.7	574	15 US-10-371-099-6	Sequence 6, Appli

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16 211 7.7 574 15 US-10-371-122-6 Sequence 6, Appli
17 211 7.7 574 15 US-10-373-567-6 Sequence 6, Appli
18 210.5 7.6 539 15 US-10-371-264-19 Sequence 19, Appl
19 210.5 7.6 539 15 US-10-371-099-315 Sequence 315, App
20 210.5 7.6 539 15 US-10-371-122-315 Sequence 315, App
21 210.5 7.6 539 15 US-10-373-567-19 Sequence 19, Appl
22 208.5 7.6 539 15 US-10-373-567-9 Sequence 9, Appli
23 208.5 7.6 539 15 US-10-371-264-18 Sequence 18, Appl
24 208.5 7.6 539 15 US-10-371-099-9 Sequence 9, Appli
25 208.5 7.6 539 15 US-10-371-099-314 Sequence 314, App
26 208.5 7.6 539 15 US-10-371-122-9 Sequence 9, Appli
27 208.5 7.6 539 15 US-10-371-122-314 Sequence 314, App
28 208.5 7.6 539 15 US-10-373-567-9 Sequence 9, Appli
29 208.5 7.6 539 15 US-10-373-567-18 Sequence 18, Appl
30 203 7.4 574 15 US-10-371-264-7 Sequence 7, Appli
31 203 7.4 574 15 US-10-371-099-7 Sequence 7, Appli
32 203 7.4 574 15 US-10-371-122-7 Sequence 7, Appli
33 203 7.4 574 15 US-10-373-567-7 Sequence 7, Appli
34 198.5 7.2 539 15 US-10-371-264-21 Sequence 21, Appl
35 198.5 7.2 539 15 US-10-371-099-317 Sequence 317, App
36 198.5 7.2 539 15 US-10-371-122-317 Sequence 317, App
37 198.5 7.2 539 15 US-10-373-567-21 Sequence 21, Appl
38 194 7.0 538 15 US-10-371-264-12 Sequence 12, Appl
39 194 7.0 538 15 US-10-371-099-12 Sequence 12, Appl
40 194 7.0 538 15 US-10-371-122-12 Sequence 12, Appl
41 194 7.0 538 15 US-10-373-567-12 Sequence 12, Appl
42 192.5 7.0 539 15 US-10-371-264-20 Sequence 20, Appl
43 192.5 7.0 539 15 US-10-371-099-316 Sequence 316, App
44 192.5 7.0 539 15 US-10-371-122-316 Sequence 316, App
45 192.5 7.0 539 15 US-10-373-567-20 Sequence 20, Appl
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ALIGNMENTS

RESULT 1

US-09-881-457A-2
; Sequence 2, Application US/09881457A

; Patent No. US20020081316A1

; GENERAL INFORMATION:

; APPLICANT: Cochran, Mark D

; APPLICANT: Cook, Stephanie M

; APPLICANT: Wild, Martha A

; TITLE OF INVENTION: No. US20020081316A1el Avian Herpes Virus and Uses Thereof

; FILE REFERENCE: SY01105K1QKQK

; CURRENT APPLICATION NUMBER: US/09/881,457A

; CURRENT FILING DATE: 2001-06-14

; PRIOR APPLICATION NUMBER: 09/426,352

; PRIOR FILING DATE: 1999-10-25

; PRIOR APPLICATION NUMBER: 08/804,372

; PRIOR FILING DATE: 1997-02-21

; PRIOR APPLICATION NUMBER: PCT/US95/10245

; PRIOR FILING DATE: 1995-08-09

; PRIOR APPLICATION NUMBER: 08/663,566

; PRIOR FILING DATE: 1996-06-13

; PRIOR APPLICATION NUMBER: 08/288,065

; PRIOR FILING DATE: 1994-08-09

; PRIOR APPLICATION NUMBER: PCT/US93/05681

; PRIOR FILING DATE: 1993-06-14

; PRIOR APPLICATION NUMBER: 08/023,610

; PRIOR FILING DATE: 1993-02-26

; PRIOR APPLICATION NUMBER: 07/898,087

; PRIOR FILING DATE: 1992-06-12

; NUMBER OF SEQ ID NOS: 5

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 2

; LENGTH: 564

; TYPE: PRT

; ORGANISM: Newcastle disease virus

; FEATURE:

; NAME/KEY: misc feature

; LOCATION: (54)-

; OTHER INFORMATION: Xaa = any amino acid

US-09-881-457A-2

Query Match 90.4%; Score 2493.5; DB 9; Length 564;
Best Local Similarity 89.7%; Pred. No. 3.2e-207;
Matches 496; Conservative 24; Mismatches 32; Indels 1; Gaps 1;

QY 1 MGRSSTRIPVPLMLTVRVALALSCVPTSSLDGRPLAAGIVTGKAVNIYTSQTGS 60
DB 13 MGRSPSTKNPAPMMLTVIRVALVLSICIPANSIDGRPLAAGXWLOETKQ-STYTPHPQV 71
QY 61 IIVKLLPNPKDKEACAKAPLEAYNRTLTLTLPGLDSIRIQSVTSSGGKGRIGLA 120
DB 72 NHKLLPNLPKDEACAKAPLDAYNRTLTLTLPGLDSIRIQSVTSSGGKGRIGLA 131
QY 121 IIGGAALGVATAAQITAAALIQANNAANILRLKERIAATNEAVHEVTDGLSOLAVG 180
DB 132 IIGGVALGVATAAQITAAALIQAKNAANILRLKESIAATNEAVHEVTDGLSOLAVG 191
QY 181 KMQQFVNDQFNKTAQELDCIKITQOVGVNELNLYLTETTVFGPQITSPALTLTIOALYN 240
DB 192 KMQQFVNDQFNKTAQELDCIKIAQQOVGVNELNLYLTETTVFGPQITSPALNKLTIQALYN 251
QY 241 LAGNMDYLLTKLGVNNQLSSLGSLITGNPILYDSQTLGLGIVTLPSVGNLNNMRA 300
DB 252 LAGNMDYLLTKLGVNNQLSSLGSLITGNPILYDSQTLGLGIVTLPSVGNLNNMRA 311
QY 301 TYLETLSVSTTKGFASALVPKVMKGVSVIBELDTSYCIETDLDLYCTRIVTFPMSPGIY 360
DB 312 TYLETLSVSTTKGFASALVPKVMKGVSVIBELDTSYCIETDLDLYCTRIVTFPMSPGIY 371
QY 361 SCLSGNTSACMYKTEGALTTPYMTLKGSVIANCKMTTCRCADPPGIISQNYGEAVSLID 420
DB 372 SCLSGNTSACMYKTEGALTTPYMTLKGSVIANCKMTTCRCADPPGIISQNYGEAVSLID 431
QY 421 RQSCNVLSLDGITLRLSGEFDATYQKNISIODSQVITVGNLDISTELGNVNNISNALDK 480
DB 432 RQSCNVLSLDGITLRLSGEFDATYQKNISIODSQVITVGNLDISTELGNVNNISNALDK 491
QY 481 LEESNKLKDNVKNLTSTTSALITYIVLTIVSLVCGILSLVACILMYKQKQAKOQKTLMLG 540
DB 492 LEESNKLKDNVKNLTSTTSALITYIVLTIVSLVCGILSLVACILMYKQKQAKOQKTLMLG 551
QY 541 NNTLDQMRATTKM 553
DB 552 NNTLDQMRATTKM 564

RESULT 2
US-10-267-682-94
Sequence 94, Application US/10267682
Publication No. US20040033235A1
GENERAL INFORMATION:
APPLICANT: Bolognesi, Dani P.
Matthews, Thomas J.
Wild, Carl T.
Barney, Shawn O.
Lambert, Dennis M.
Pettaway, Stephen R.
Langlois, Alphonse J.

TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF
MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING HIV
TRANSMISSION

NUMBER OF SEQUENCES: 239
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
APPLICANT: Pennie & Edmonds
FILING DATE: 08-Oct-2002
CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/484,223A
FILING DATE: 07-JUN-1995

ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7872-029

TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE

INFORMATION FOR SEQ ID NO: 94:
SEQUENCE CHARACTERISTICS:
LENGTH: 436 amino acids
TYPE: amino acid

STRANDEDNESS: <Unknown>
TOPOLOGY: unknown
MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 94:
US-10-267-682-94

Query Match 75.7%; Score 2086.5; DB 12; Length 436;
Best Local Similarity 96.6%; Pred. No. 4.3e-172;
Matches 421; Conservative 2; Mismatches 12; Indels 1; Gaps 1;

QY 118 IGATIGGAALGVATAAQITAAALIQANNAANILRLKERIAATNEAVHEVTDGLSOLAV 177
DB 2 IGATIGGAALGVATAAQITAAALIQANNAANILRLKESITATIEAVHEVTDGLSOLAV 61
QY 178 AVGRMQQFVNDQFNKTAQELDCIKITQOVGVNELNLYLTETTVFGPQITSPALTLTIOA 237
DB 62 AVGRMQQFVNDQFNKTAQELDCIKITQOVGVNELNLYLTETTVFGPQITSPALTLTIOA 121
QY 238 LYNLAGNMDYLLTKLGVNNQLSSLGSLITGNPILYDSQTLGLGIVTLPSVGNLNN 297
DB 122 LYN-AGNMDYLLTKLGVNNQLSSLGSLITGNPILYDSQTLGLGIVTLPSVGNLNN 180
QY 298 MRATYLETLSVSTTKGFASALVPKVMKGVSVIBELDTSYCIETDLDLYCTRIVTFPMSP 357
DB 181 MRATYLETLSVSTTKGFASALVPKVMKGVSVIBELDTSYCIETDLDLYCTRIVTFPMSP 240
QY 358 GIYSCLSGNTSACMYKTEGALTTPYMTLKGSVIANCKMTTCRCADPPGIISQNYGEAVS 417
DB 241 GIYSCLSGNTSACMYKTEGALTTPYMTLKGSVIANCKMTTCRCADPPGIISQNYGEAVS 300
QY 418 LIDRQSCNVLSLDGITLRLSGEFDATYQKNISIODSQVITVGNLDISTELGNVNNISNA 477
DB 301 LIDRQSCNVLSLDGITLRLSGEFDATYQKNISIODSQVITVGNLDISTELGNVNNISNA 360
QY 478 LDKLEESNKLKDNVKNLTSTTSALITYIVLTIVSLVCGILSLVACILMYKQKQAKOQKTL 537
DB 361 LDKLEESNKLKDNVKNLTSTTSALITYIVLTIVSLVCGILSLVACILMYKQKQAKOQKTL 420
QY 538 WLGNNTLQMRATTKM 553
DB 421 WLGNNTLQMRATTKM 436

RESULT 3
US-10-267-748-94
Sequence 94, Application US/10267748
Publication No. US20040052820A1
GENERAL INFORMATION:
APPLICANT: Bolognesi, Dani P.
Matthews, Thomas J.
Wild, Carl T.
Barney, Shawn O.

Lambert, Dennis M.
Petteway, Stephen R.
Langlois, Alphonse J.
TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF
MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING HIV
TRANSMISSION
NUMBER OF SEQUENCES: 239
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/267,748
FILING DATE: 08-Oct-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/484,223A
FILING DATE: 07-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7872-029
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
INFORMATION FOR SEQ ID NO: 94:
SEQUENCE CHARACTERISTICS:
LENGTH: 436 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: unknown
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 94:
US-10-267-748-94
Query Match 75.7%; Score 2086.5; DB 12; Length 436;
Best Local Similarity 96.6%; Pred. No. 4.3e-172;
Matches 421; Conservative 2; Mismatches 12; Indels 1; Gaps 1;
QY 118 IGAIIGGAALGVATAAQITTAASALIQANQNAANTILRLKERTATNEAVHEVTDGLSOLAV 177
DB 2 IGAIIGSVALGVATAAQITTAASALIQANQNAANTILRLKESITATIEAVHEVTDGLSOLAV 61
QY 178 AVGRMQQFVNDQFNKTAQELDCIKITQGVGVELNLYLTETTVFGPOITSPALFQLTIQA 237
DB 62 AVGRMQQFVNDQFNKTAQELDCIKITQGVGVELNLYLTETTVFGPOITSPALFQLTIQA 121
QY 238 LYNLAGNMDYLLTKLGVGNQNLSSLGSLITGNPILYDSQTLGLIQVTLPSVGNLNN 297
DB 122 LYN-AGNMDYLLTKLGVGNQNLSSLGSLITGNPILYDSQTLGLIQVTLPSVGNLNN 180
QY 298 MRATYLETSLVSTTKGFASALVPKVMKGVSVIEELDTSCYCIETDLDLYCTRIYTFPMSP 357
DB 181 MRATYLETSLVSTTKGFASALVPKVMKGVSVIEELDTSCYCIETDLDLYCTRIYTFPMSP 240
QY 358 GIYCLSGNTSACMYSKTEGALTTPYMTLKGSVIANCKWTTTCRCADPPGIISQNYGEAVS 417
DB 241 GIYCLSGNTSACMYSKTEGALTTPYMTLKGSVIANCKWTTTCRCADPPGIISQNYGEAVS 300
QY 418 LIDRQCNVLSLDGTTILSLGFEFDATYQKNISIQDSQVIVTGNLIDISTELGNVNNISNA 477
DB 301 LIDRQCNVLSLDGTTILSLGFEFDATYQKNISILDSQVIVTGNLIDISTELGNVNNISNA 360
QY 478 LDKLEESNKLKVNKVLTSALITYIVLTVISLVCILSLVLAACYLMYKQKQKQKTL 537

DB 361 LDKLEESNKLKVNKVLTSALITYIVLTVISLVCILSLVLAACYLMYKQKQKQKTL 420
QY 538 WLGNNTLDQMRATTKM 553
DB 421 WLGNNTLDQMRATTKM 436
RESULT 4
US-09-951-061A-141
; Sequence 141, Application US/09951061A
; Publication No. US20030082204A1
; GENERAL INFORMATION:
; APPLICANT: Paoletti, Enzo
; APPLICANT: Tartaglia, James
; APPLICANT: Taylor, Jill
; APPLICANT: Gettig, Russell
; TITLE OF INVENTION: POXVIRUS - CANINE DISTEMPER VIRUS (CDV)
; TITLE OF INVENTION: RECOMBINANTS AND COMPOSITIONS AND METHODS EMPLOYING THE
; TITLE OF INVENTION: RECOMBINANTS
; NUMBER OF SEQUENCES: 143
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: McDonnell, Boehnen, Hulbert & Berghoff
; STREET: 300 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States of America
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/951,061A
; FILING DATE: 13-SEP-2001
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 09/354,138
; FILING DATE: 15-JUL-1999
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/224,657
; FILING DATE: 16-APR-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/073,962
; FILING DATE: 08-JUN-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/776,867
; FILING DATE: 23-OCT-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/621,614
; FILING DATE: 30-NOV-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/938,283
; FILING DATE: 31-AUG-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/621,614
; FILING DATE: 30-NOV-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/105,483
; FILING DATE: 12-AUG-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/847,951
; FILING DATE: 06-MAR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/713,967
; FILING DATE: 11-JUN-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07,666,056
; FILING DATE: 07-MAR-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Frommer, William S.
; REGISTRATION NUMBER: 25,506
; REFERENCE/DOCKET NUMBER: 454310-2860

TELECOMMUNICATION INFORMATION:
 TELEPHONE: (212) 840-3333
 TELEFAX: (212) 840-0712
 INFORMATION FOR SEQ ID NO: 141:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 662 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: Peptide
 FRAGMENT TYPE: internal
 US-09-951-061A-141

Query Match 22.6%; Score 623.5; DB 10; Length 662;
 Best Local Similarity 27.3%; Pred. No. 6.4e-45;

Matches 143; Conservative 120; Mismatches 249; Indels 11; Gaps 5;

```

QY 19 VALALSCVCPSSLDGRPLAAGIVVTGDKAVNIYTSSTGSIIVKLLPNPKDEACAK 78
Db 124 LGMASLFLCSKAQHWNLSITIGITDGVHYKIMTRPSHQVLYIKLMPNVSL-LENCTK 182
QY 79 APLEAYNRTLTLLTPLDGSIIRIQESV----TTSGGGKQGRLLIGALIGGALGVATAAQ 134
Db 183 AELGEYKLLSVLEPINOALMTKNVKKPLQSLGSGRRQRRFAGVILAGVATAAQ 242
QY 135 ITAASALIQANQNAANILRLKERIAATNEAVHEVTDGLSOLAVAGKMQQFVNDQFNKTA 194
Db 243 ITAGIALHQSNLNAQAIOQLRSLTSLEQSNKAIEETREATQETVIAVQGVQDYVNNELVPAM 302
QY 195 QELDCIKITQGVVELNLYLTETLTVFGPQITSPALTOITQALYNLAGNMDYLLTKLG 254
Db 303 QHMSCELVGQRLGLRLRYTTELLSIFGSLRDPISAEISIQALIYALGGEIHKILKLG 362
QY 255 VGNQLSLSGLITGNPILYDSQTQLLGIQVTLPSVGNLNNMRATVLETLSVSTTKGF 314
Db 363 YSGDMTALLESRGKTKITHVDLPFGKFIILSYPTLSEVKGVIHVRLEAVSNIGSQE 422
QY 315 ASALVPKVMKGVSVIEELDTSYCIETDLDLYCTRIVTFPMSPGIYSCLSGNTSACMYSK 374
Db 423 WYTTVPRIATNGVLIISNFDSESCVFSAEISALCONSLYPMSPLQOCIRGDTSCARTL 482
QY 375 TEGALTTPYMTLKSIVANCMWTCRCADPPGIISQNYGEAVSLDRQSCNVLSDGHTL 434
Db 483 VSGTMGNKFLSKGNIVANCASILCKCVSTSTIINQSPDKLLTFIASDTCPLVEIDGATI 542
QY 435 RLSGEF--DATYQKNISIQDSQVITVGNLDISTELGNVNNISNALOKLEESNKLKDVN 492
Db 543 QVGRQVPDMVYEGKVAL--GPAISLDRLDVGTLNGLAKLDDDAKVLIDSSNQILETVR 600
QY 493 VKLTSTGALITYIVLTVISLVCGILSLVLAACYLMYKQKQOKT 535
Db 601 RSSFNFGSLLSVPILSCTAL--ALLLLIYCKRRYQOTLKQHT 641

```

RESULT 5

US-10-670-695-36

Sequence 36, Application US/10670695

Publication No. US20040058316A1

GENERAL INFORMATION:

APPLICANT: Jensen, Wayne A.

APPLICANT: Lappin, Michael R.

APPLICANT: Rosen, David K.

APPLICANT: Andrews, Janet S.

TITLE OF INVENTION: USE OF RECOMBINANT ANTIGENS TO DETERMINE THE IMMUNE

FILE REFERENCE: DI-9-1

CURRENT APPLICATION NUMBER: US/10/670,695

CURRENT FILING DATE: 2003-09-25

PRIOR APPLICATION NUMBER: 09/521,738

PRIOR FILING DATE: 2000-03-09

NUMBER OF SEQ ID NOS: 36

SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO 36

LENGTH: 662

TYPE: PRT

ORGANISM: canine distemper virus

US-10-670-695-36

Query Match

Best Local Similarity 22.5%; Score 621.5; DB 12; Length 662;

Matches 143; Conservative 120; Mismatches 249; Indels 11; Gaps 5;

```

QY 19 VALALSCVCPSSLDGRPLAAGIVVTGDKAVNIYTSSTGSIIVKLLPNPKDEACAK 78
Db 124 LGMASLFLCSKAQHWNLSITIGITDGVHYKIMTRPSHQVLYIKLIPNASL-LENCTK 182
QY 79 APLEAYNRTLTLLTPLDGSIIRIQESV----TTSGGGKQGRLLIGALIGGALGVATAAQ 134
Db 183 AELGEYKLLSVLEPINOALMTKNVKKPLQSLGSGRRQRRFAGVILAGVATAAQ 242
QY 135 ITAASALIQANQNAANILRLKERIAATNEAVHEVTDGLSOLAVAGKMQQFVNDQFNKTA 194
Db 243 ITAGIALHQSNLNAQAIOQLRSLTSLEQSNKAIEETREATQETVIAVQGVQDYVNNELVPAM 302
QY 195 QELDCIKITQGVVELNLYLTETLTVFGPQITSPALTOITQALYNLAGNMDYLLTKLG 254
Db 303 QHMSCELVGQRLGLRLRYTTELLSIFGSLRDPISAEISIQALIYALGGEIHKILKLG 362
QY 255 VGNQLSLSGLITGNPILYDSQTQLLGIQVTLPSVGNLNNMRATVLETLSVSTTKGF 314
Db 363 YSGDMTALLESRGKTKITHVDLPFGKFIILSYPTLSEVKGVIHVRLEAVSNIGSQE 422
QY 315 ASALVPKVMKGVSVIEELDTSYCIETDLDLYCTRIVTFPMSPGIYSCLSGNTSACMYSK 374
Db 423 WYTTVPRIATNGVLIISNFDSESCVFSAEISALCONSLYPMSPLQOCIRGDTSCARTL 482
QY 375 TEGALTTPYMTLKSIVANCMWTCRCADPPGIISQNYGEAVSLDRQSCNVLSDGHTL 434
Db 483 VSGTMGNKFLSKGNIVANCASILCKCVSTSTIINQSPDKLLTFIASDTCPLVEIDGATI 542
QY 435 RLSGEF--DATYQKNISIQDSQVITVGNLDISTELGNVNNISNALOKLEESNKLKDVN 492
Db 543 QVGRQVPDMVYEGKVAL--GPAISLDRLDVGTLNGLAKLDDDAKVLIDSSNQILETVR 600
QY 493 VKLTSTGALITYIVLTVISLVCGILSLVLAACYLMYKQKQOKT 535
Db 601 RSSFNFGSLLSVPILSCTAL--ALLLLIYCKRRYQOTLKQHT 641

```

RESULT 6

US-09-873-233A-20

Sequence 20, Application US/09873233A

Patent No. US20020146434A1

GENERAL INFORMATION:

APPLICANT: UEDA, Shigeharu

APPLICANT: WATANABE, Michiko

APPLICANT: KAWANISHI, Hitomi

TITLE OF INVENTION: GENE CODING FOR THE MEASLES VIRUS MUTANT ANTIGEN

FILE REFERENCE: 0216-0451P

CURRENT APPLICATION NUMBER: US/09/873,233A

CURRENT FILING DATE: 2001-06-05

NUMBER OF SEQ ID NOS: 32

SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO 20

LENGTH: 550

TYPE: PRT

ORGANISM: Measles virus

FEATURE:

NAME/KEY: UNSURE

LOCATION: (1)..(550)

OTHER INFORMATION: any n or Xaa = Unknown

US-09-873-233A-20

Query Match

Best Local Similarity 22.0%; Score 606.5; DB 9; Length 550;

Matches 148; Conservative 118; Mismatches 245; Indels 13; Gaps 7;

QY 17 VRVALASCVCPTSSLDGRFLAAGIVVTGDKAVNIYTSQTGSIIVKLLPNMPKKEAC 76
DB 10 ILMAVLLTLQPTGQIHGNSLKGIVGVIGSASVKWTRSSHQSLVTKLMPNITL-LNNC 68
QY 77 AKAPLEAYNRTLTLLTPGDSIRIOESV-----TTSGGKGQRLGAIIGGALGVATA 132
DB 69 TRVEIAEYRLLRTVLEPIRDALNMTQNIQRPVQSVASSRRHRKRFAGVWLAGAALGVATA 128
QY 133 AQITAAASALIQANQANAILRLKERIAATNEAHEVTDGLSOLAVAGKMQQFVNDQFNK 192
DB 129 AQITAGIALHQSMLNSQALDNLRLASLETNQATEAIRQAGQEMILAVQGVQDIYNELIP 188
QY 193 TAGELDCIKITQOVGBELNYLTETLVFQPOITSPTALQTLTQALYNLAGNMDYLLTK 252
DB 189 SMQSLCDLIGQKGLKRLRYTEILSLFGPSLRDPISAEISIQALSVALGDKINKVLEK 248
QY 253 LGVGNNSLSLIGSLITGNPILYDSOTQLLGIQVTLPSVGNLNNMREATVLETLVSVTTK 312
DB 249 LGVSGDGLLGILSRGKARITHVDTESYFVLSTAYPTLSBKGVVHRLGVSNIGS 308
QY 313 GFASALPKVVMKGVSVIELDTSYCIETDLDTCTRIYVTPMSPGIVSCLSGNTSACMY 372
DB 309 QEWTTVPKYVATQGYLISNFDSECTFMEPGTVCSQNALYPMSPLQECCLRGSTKSCAR 368
QY 373 SKTEGALTTPMVLKGVSVIANCKMTTCRCADPPGIIISQNGEAVSLIDRQSCNVLSLDGI 432
DB 369 TLVSGSFGNRFILSQGNLIANCASILCKCHTTGTIINQDPDKILTYAADHCPVVEVNGV 428
QY 433 TLRLSGEF--DATYQKNISIQDSQVIVTGNLDISTELGNVNNISNALDKLEESNKLDK 490
DB 429 TIQVGSRRYPDAVYLHRIDL--GPPISLERLDVGTNLGNIAKLEDAKELLESSDQILRS 486
QY 491 VNVKLITSALITYIVLTV--ISLVCGLISLVLACVLMYKQKAAQ 533
DB 487 MK-GLSSTS--IVYLLIAVCLGLIGIPALICCCRCGRNKGEG 527

RESULT 7
US-09-873-233A-18
; Sequence 18, Application US/09873233A
; Patent No. US20020146434A1
; GENERAL INFORMATION:
; APPLICANT: UEDA, Shigeharu
; APPLICANT: WATANABE, Michiko
; APPLICANT: KAWANISHI, Hitomi
; TITLE OF INVENTION: GENE CODING FOR THE MEASLES VIRUS MUTANT ANTIGEN
; FILE REFERENCE: 0216-0451P
; CURRENT APPLICATION NUMBER: US/09/873,233A
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 18
; LENGTH: 550
; TYPE: PRT
; ORGANISM: Measles virus
; FEATURE:
; NAME/KEY: UNSURE
; LOCATION: (1)..(550)
; OTHER INFORMATION: any n or xaa = Unknown
US-09-873-233A-18

Query Match 22.0%; Score 605.5; DB 9; Length 550;
Best Local Similarity 28.5%; Pred. No. 1.8e-43;
Matches 149; Conservative 116; Mismatches 244; Indels 13; Gaps 7;
QY 19 VALALSCVCPTSSLDGRFLAAGIVVTGDKAVNIYTSQTGSIIVKLLPNMPKKEAC 78
DB 12 MAVLLTLQPTGQIHGNSLKGIVGVIGSASVKWTRSSHSHSLVTKLMPNITL-LNNCTR 70
QY 79 APLEAYNRTLTLLTPGDSIRIOESV-----TTSGGKGQRLGAIIGGALGVATAAQ 134
DB 71 VEIAEYRLLRTVLEPIRDALNMTQNIQRPVQSVASSRRHRKRFAGVWLAGAALGVATAAQ 130

QY 135 ITAASALIQANQANAILRLKERIAATNEAHEVTDGLSOLAVAGKMQQFVNDQFNKTA 194
DB 131 ITAGIALHQSMLNSQALDNLRLASLETNQATEAIRQAGQEMILAVQGVQDIYNELIPSM 190
QY 195 QELDCIKITQOVGBELNYLTETLVFQPOITSPTALQTLTQALYNLAGNMDYLLTKLG 254
DB 191 NQUSCDLIGQKGLKRLRYTEILSLFGPSLRDPISAEISIQALSVALGDKINKVLEKLG 250
QY 255 VGNQNSLSLIGSLITGNPILYDSOTQLLGIQVTLPSVGNLNNMREATVLETLVSVTTKGF 314
DB 251 YSGDGLLGILSRGKARITHVDTESYFVLSTAYPTLSBKGVVHRLGVSNIGSQE 310
QY 315 ASALPKVVMKGVSVIELDTSYCIETDLDTCTRIYVTPMSPGIVSCLSGNTSACMYSK 374
DB 311 WYTTVPKYVATQGYLISNFDSECTFMEPGTVCSQNALYPMSPLQECCLRGFTKSCARTL 370
QY 375 TEGALTTPMVLKGVSVIANCKMTTCRCADPPGIIISQNGEAVSLIDRQSCNVLSLDGITL 434
DB 371 VSGSFGNRFILSQGNLIANCASILCKCHTTGTIINQDPDKILTYAADHCPVVEVNGVTI 430
QY 435 RLSGEF--DATYQKNISIQDSQVIVTGNLDISTELGNVNNISNALDKLEESNKLDKVN 492
DB 431 QVGSRRYPDAVYLHRIDL--GPPISLERLDVGTNLGNIAKLEDAKELLESSDQILRSKM 488
QY 493 VKLITSALITYIVLTV--ISLVCGLISLVLACVLMYKQKAAQ 533
DB 489 -GLSSTS--IVYLLIAVCLGLIGIPALICCCRCGRNKGEG 527

RESULT 8
US-10-267-682-93
; Sequence 93, Application US/10267682
; Publication No. US2004003235A1
; GENERAL INFORMATION:
; APPLICANT: Bolognesi, Dani P.
; Matthews, Thomas J.
; Wild, Carl T.
; Barney, Shawn O.
; Lambert, Dennis M.
; Petteway, Stephen R.
; Langlois, Alphonse J.
; TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF
; MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING HIV
; TRANSMISSION
; NUMBER OF SEQUENCES: 239
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/267,682
; FILING DATE: 08-Oct-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/484,223A
; FILING DATE: 07-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A.
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 7872-029
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE

INFORMATION FOR SEQ ID NO: 93:
SEQUENCE CHARACTERISTICS:
LENGTH: 438 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: unknown
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 93:
US-10-267-682-93

Query Match 19.4%; Score 534; DB 12; Length 438;
Best Local Similarity 28.2%; Pred. No. 2e-37;
Matches 118; Conservative 97; Mismatches 198; Indels 6; Gaps 3;
119 GAIIAGALGVATAQAIIAASALIQANQANAMILKRIATNEAVHVTGLQLAVA 178
3 GVVLGVALGVATAQAIIAGIALHQSNLNAQAIOQLRTSLQSNKAIEIREATQETVIA 62
179 VKMQOQFVNDQFNKTAQELDCIKITQQGVVELNLVLTTLTVFGPOITSPALTLQIAL 238
63 VQGVQDYNNELVPMQHMSELVQRLGLRLRYVTELLSIFGSLRDPISAEISIAL 122
239 YNLAGNNDYLLTKLGVGNQLSSILGSLITGNPILYDSQTLGLGIQVTLPSVGNLNM 298
123 IYALGGEHKLKLGKYGSGDMAILESRIKTHVDLPKGFILSISYPTLSEVKG 182
299 RATYLETSLVSTTKGFASALVPKVMKGVSVIEELDTSYCIETDLDLYCTRIVTPMSPG 358
183 IVHREAVSYNGSQEWYTVPRYATNGYLINSFDESSCVFVSESAICSONSLYPMSP 242
359 IYSLGSGNTSACMYSKTEGALTTPYMTLKGSIANCKMTTCRCADPPGIISONVGEAVSL 418
243 LQCCIRGDTSSCARTLVSGTMGNKFIKSGNIVANCASILCKCYSTSTIINQSPDKLTF 302
419 IDROSCNVLSLDGTLRLSGEF--DATYKKNISIQDSQVIVTGNLDISTELGNVNSISN 476
303 IASDTCPVIEDGATIQVGRQYPMVYEGKVAL--GPAISLDRLDVGNTLGNALKKLD 360
477 ALDKLEESNKLKNNVLTSTALITVILTVISLVGILSLVLAACYLVMYKQKQAKT 535
361 AKVLIDSSNQILETVRRSSFNFGSLSPILSCTAL--ALLLIYCKRRYQQTILKQHT 417

RESULT 9

US-10-267-748-93
Sequence 93, Application US/10267748
Publication No. US20040052820A1

GENERAL INFORMATION:

APPLICANT: Bolognesi, Dani P.
Matthews, Thomas J.
Wild, Carl T.
Barney, Shawn O.
Lambert, Dennis M.
Pettaway, Stephen R.
Langlois, Alphonse J.

TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF
MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING HIV
TRANSMISSION

NUMBER OF SEQUENCES: 239

CORRESPONDENCE ADDRESS:

ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036-2711

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/267,748

FILING DATE: 08-Oct-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/484,223A
FILING DATE: 07-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7872-029
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 93:
SEQUENCE CHARACTERISTICS:
LENGTH: 438 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: unknown
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 93:
US-10-267-748-93

Query Match 19.4%; Score 534; DB 12; Length 438;
Best Local Similarity 28.2%; Pred. No. 2e-37;
Matches 118; Conservative 97; Mismatches 198; Indels 6; Gaps 3;
119 GAIIAGALGVATAQAIIAASALIQANQANAMILKRIATNEAVHVTGLQLAVA 178
3 GVVLGVALGVATAQAIIAGIALHQSNLNAQAIOQLRTSLQSNKAIEIREATQETVIA 62
179 VKMQOQFVNDQFNKTAQELDCIKITQQGVVELNLVLTTLTVFGPOITSPALTLQIAL 238
63 VQGVQDYNNELVPMQHMSELVQRLGLRLRYVTELLSIFGSLRDPISAEISIAL 122
239 YNLAGNNDYLLTKLGVGNQLSSILGSLITGNPILYDSQTLGLGIQVTLPSVGNLNM 298
123 IYALGGEHKLKLGKYGSGDMAILESRIKTHVDLPKGFILSISYPTLSEVKG 182
299 RATYLETSLVSTTKGFASALVPKVMKGVSVIEELDTSYCIETDLDLYCTRIVTPMSPG 358
183 IVHREAVSYNGSQEWYTVPRYATNGYLINSFDESSCVFVSESAICSONSLYPMSP 242
359 IYSLGSGNTSACMYSKTEGALTTPYMTLKGSIANCKMTTCRCADPPGIISONVGEAVSL 418
243 LQCCIRGDTSSCARTLVSGTMGNKFIKSGNIVANCASILCKCYSTSTIINQSPDKLTF 302
419 IDROSCNVLSLDGTLRLSGEF--DATYKKNISIQDSQVIVTGNLDISTELGNVNSISN 476
303 IASDTCPVIEDGATIQVGRQYPMVYEGKVAL--GPAISLDRLDVGNTLGNALKKLD 360
477 ALDKLEESNKLKNNVLTSTALITVILTVISLVGILSLVLAACYLVMYKQKQAKT 535
361 AKVLIDSSNQILETVRRSSFNFGSLSPILSCTAL--ALLLIYCKRRYQQTILKQHT 417

RESULT 10

US-10-267-682-105
Sequence 105, Application US/10267682
Publication No. US20040033235A1

GENERAL INFORMATION:

APPLICANT: Bolognesi, Dani P.
Matthews, Thomas J.
Wild, Carl T.
Barney, Shawn O.
Lambert, Dennis M.
Pettaway, Stephen R.
Langlois, Alphonse J.

TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF

MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING HIV
TRANSMISSION

NUMBER OF SEQUENCES: 239

CORRESPONDENCE ADDRESS:

```

; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/267,682
; FILING DATE: 08-Oct-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/484,223A
; FILING DATE: 07-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A.
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 7872-029
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 105:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 438 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 105:
US-10-267-682-105

Query Match      18.3%; Score 504; DB 12; Length 438;
Best Local Similarity 29.7%; Pred. No. 7.8e-35;
Matches 124; Conservative 91; Mismatches 195; Indels 8; Gaps 5;

QY 119 GAIIGGAALGVATAAQAITAASALIQANQNAANILRLKERIAATNEAVEHVTGGLSQLAVA 178
DB 3 GVVLAGAALGVATAAQAITAGIALHQSMNSQADNLRASLETNNQAEARQAGQEMILA 62
QY 179 VGRMQQFVNDQFNKTAQELDCIKITQQGVVELNLYLTETLTTFVGPQITSPALQTTOAL 238
DB 63 VQGVQDYINNELIPSMNQLSCDLIGQKLGKLLRYTTEILSLFGPSLRDPISEISQAL 122
QY 239 YNLAGNMVLLTKLGVGNQNLSSLGSLITGNPILYDSQTQLLGLGQVTLPSVGNLNM 298
DB 123 SYALGGDINKVLEKLGYSGGDLGILSRGKARIKTHVDTESYFIVLSIAYPTLSEIKGV 182
QY 299 RATYLETLVSSTTKGFASALVPKVMKGVSVIEELDTSYCIETDLDLYCTRIVTFPMSPG 358
DB 183 IVHRELGVSINIGQEWYTPVKVATQGYLISNFDSESCTFMPEGVCSQNALYPMSP 242
QY 359 IYSLSGNTSACMYSKTEGALTTPYMTLKGSVIANCKMTTCRCADPPGIISQNYGEAVSL 418
DB 243 LQELRGSTKSCARTLVSGSGFGRFILSQGNLIANCASILCKCYTTGTTIINQDPDKILTY 302
QY 419 IDRQSCNVLSDGTLRLSGEF--DATYQKNISIQDSQVITVGNLDISTELGNVNNISN 476
DB 303 IAAHCFVWVGVTIQVGSRRYPDAVYLHRRIDL--GPPISLERLDVGTNLGNIAKLED 360
QY 477 ALDKLEESNKLKDVNKLSTSLALITVITV--ISLVCGILSILVLAACYLMYKQAKQ 533
DB 361 AKELLESQDLRLSMK--GLSSTS--IYVILIAVCLGLGILGIPALICCRGRCNKKGEQ 415

RESULT 11
US-10-267-748-105
; Sequence 105, Application US/10267748
; Publication No. US20040052820A1
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; GENERAL INFORMATION:
; APPLICANT: Bolognesi, Dani P.
; Matthews, Thomas J.
; Wild, Carl T.
; Barney, Shawn O.
; Lambert, Dennis M.
; Petteway, Stephen R.
; Langlois, Alphonse J.
; TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF
; MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING HIV
; TRANSMISSION
; NUMBER OF SEQUENCES: 239
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/267,748
; FILING DATE: 08-Oct-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/484,223A
; FILING DATE: 07-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A.
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 7872-029
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 105:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 438 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 105:
US-10-267-748-105

Query Match      18.3%; Score 504; DB 12; Length 438;
Best Local Similarity 29.7%; Pred. No. 7.8e-35;
Matches 124; Conservative 91; Mismatches 195; Indels 8; Gaps 5;

QY 119 GAIIGGAALGVATAAQAITAASALIQANQNAANILRLKERIAATNEAVEHVTGGLSQLAVA 178
DB 3 GVVLAGAALGVATAAQAITAGIALHQSMNSQADNLRASLETNNQAEARQAGQEMILA 62
QY 179 VGRMQQFVNDQFNKTAQELDCIKITQQGVVELNLYLTETLTTFVGPQITSPALQTTOAL 238
DB 63 VQGVQDYINNELIPSMNQLSCDLIGQKLGKLLRYTTEILSLFGPSLRDPISEISQAL 122
QY 239 YNLAGNMVLLTKLGVGNQNLSSLGSLITGNPILYDSQTQLLGLGQVTLPSVGNLNM 298
DB 123 SYALGGDINKVLEKLGYSGGDLGILSRGKARIKTHVDTESYFIVLSIAYPTLSEIKGV 182
QY 299 RATYLETLVSSTTKGFASALVPKVMKGVSVIEELDTSYCIETDLDLYCTRIVTFPMSPG 358
DB 183 IVHRELGVSINIGQEWYTPVKVATQGYLISNFDSESCTFMPEGVCSQNALYPMSP 242
QY 359 IYSLSGNTSACMYSKTEGALTTPYMTLKGSVIANCKMTTCRCADPPGIISQNYGEAVSL 418
DB 243 LQELRGSTKSCARTLVSGSGFGRFILSQGNLIANCASILCKCYTTGTTIINQDPDKILTY 302
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QY 419 IDRCNVLSLDGTLRLSGF--DATYQKNISIODSQVIVTGNLDISTELGNVNNISN 476
DB 303 IADHCPVVEVNGVTVQVSRYPYAVLHRDL--GPFISLERLDVGTNLGNATAKUED 360
QY 477 ALDKLEESNSKLDKVVNKLITSTSLITYIVLTV--ISLVCGILSLVLACYLMTYKQKAAQ 533
DB 361 AKELLESSDQILRSKM--GLSSTS--IVYILIAVCLGLGIGIPALICCCRCGRCKRKEQ 415

RESULT 12

US-10-267-682-95
; Sequence 95, Application US/10267682
; Publication No. US20040033235A1
; GENERAL INFORMATION:
; APPLICANT: Bolognesi, Dani P.
; Matthews, Thomas J.
; Wild, Carl T.
; Barney, Shawn O.
; Lambert, Dennis M.
; Petteway, Stephen R.
; Langlois, Alphonse J.
; TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF
; MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING HIV
; TRANSMISSION
; NUMBER OF SEQUENCES: 239
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/267,682
; FILING DATE: 08-Oct-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/484,223A
; FILING DATE: 07-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A.
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 7872-029
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 95:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 430 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 95:

US-10-267-682-95
Query Match 16.6%; Score 458; DB 12; Length 430;
Best Local Similarity 27.6%; Pred. No. 7,4e-31;
Matches 118; Conservative 81; Mismatches 219; Indels 10; Gaps 1;
QY 119 GAITGAGLVATQAQITAGALQANQANILRLKRIATNEAVHEVTDGLSQLAVA 178
DB 3 GGVIQTALGVATQAQITAAVALVEAKQARSDEIKLKEAIRDTNKAQVQSSIGNLIVA 62
QY 179 VGKMQQVNDQFNKTAQELDCIKITQQVGVNLVLTITVFGPQITSPALTOITQAL 238
DB 63 IKSVDYVKNKEIVPSIARLGCEAGLQLGIALTOHYSELTNIFGDNIGLSQEKGLQGI 122

QY 239 YNLAGNNMDYLLTKLGVNNQSSILGSLITGNPILYDSQTQLLIGIQVTLPSVGNLNNM 298
DB 123 ASLYRNTITEPTTSTVDKIDYIDLLFTESIKVRVIDVLDNDYSITLQVRLPLLTLLNT 182
QY 299 RATYLETISVSTTKGFASALVPKVMKGVSVLEELDTSYCIETDLDLYCTRIVTTPMSG 358
DB 183 QIYRVDSISYNIQNRWIPLPFSHMTKGAFILGGADVKECEIAFSSYICPSDPGFVINHE 242
QY 359 IYSCLSGNTSACMYSKTEGALTTPYMTLKGSVIANCKMTTCRCADPPGIISQNYGEAVSL 418
DB 243 MESCLSGNISQCPRTVVKSDIVPRYAFVNGGVVANCITTTCTCNGIGNRINQPPDOGVKI 302
QY 419 IDRCNVLSLDGTLRLSGFDTATYQKNISIODSQVIVTGNLDISTELGNVNNISNAL 478
DB 303 ITHKECNTIGINGMLFNTNKEGTAFYTPNDITLNSVALDPIDISIELNKAKSLESK 362
QY 479 DKLEESNSKLDKVVNKLITSTSLITYIVLTVISLVCGILSLVLACYLMTYKQKAAQKTLW 538
DB 363 EWIRSNQKLSIGNWHQSSTIIIVLIMILFIINTVIIIAVYRIQK----- 414
QY 539 LGNNTLDQ 546
DB 415 --RNRVDQ 420

RESULT 13

US-10-267-748-95
; Sequence 95, Application US/10267748
; Publication No. US20040052820A1
; GENERAL INFORMATION:
; APPLICANT: Bolognesi, Dani P.
; Matthews, Thomas J.
; Wild, Carl T.
; Barney, Shawn O.
; Lambert, Dennis M.
; Petteway, Stephen R.
; Langlois, Alphonse J.
; TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF
; MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING HIV
; TRANSMISSION
; NUMBER OF SEQUENCES: 239
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/267,748
; FILING DATE: 08-Oct-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/484,223A
; FILING DATE: 07-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A.
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 7872-029
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 95:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 430 amino acids
; TYPE: amino acid


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; STRANDEDNESS: <Unknown>
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 95:
US-10-267-748-95

Query Match      16.6%; Score 458; DB 12; Length 430;
Best Local Similarity 27.6%; Pred. No. 7.4e-31;
Matches 118; Conservative 81; Mismatches 219; Indels 10; Gaps 1;

QY 119 GAIIGGAALGVATAAQAIIAASAL-IAQANQANAIILRLKERIAATNEAV 178
DB 119 GAIIGGAALGVATAAQAIIAASAL-IAQANQANAIILRLKERIAATNEAV 178
QY 179 VGRNQFVNDQFNKTAQELDCIKITQQGVVGLNLYLTETLTVFGPQITSPALTIQAL 238
DB 179 VGRNQFVNDQFNKTAQELDCIKITQQGVVGLNLYLTETLTVFGPQITSPALTIQAL 238
QY 63 IKSQVQVYVKEIIVPSIARLGEAAAGLQGLIATLQHYSELINIFGDNIGSLQEKIGLQGI 122
DB 63 IKSQVQVYVKEIIVPSIARLGEAAAGLQGLIATLQHYSELINIFGDNIGSLQEKIGLQGI 122
QY 239 YNLAGNMDYLLTKLGVGNQSLSLGSLTGPNILYDSQTQLLGHIOVTLPSVGNLNM 298
DB 239 YNLAGNMDYLLTKLGVGNQSLSLGSLTGPNILYDSQTQLLGHIOVTLPSVGNLNM 298
QY 123 ASLYRTNITIFTTSTYDKYDIYDLFTBSIKVRVIDVDLNDYSITLQVRLPLRLTLNT 182
DB 123 ASLYRTNITIFTTSTYDKYDIYDLFTBSIKVRVIDVDLNDYSITLQVRLPLRLTLNT 182
QY 299 RATVLETLSVTTKGFASALVPKVMKGVSVIEBELDTSYCIETDLCTRIVTEPMSPG 358
DB 299 RATVLETLSVTTKGFASALVPKVMKGVSVIEBELDTSYCIETDLCTRIVTEPMSPG 358
QY 183 QIVRVDISINIQREWIPLPSHINTKGFAGADVKECIAFSSYICSPDPCFVLNHE 242
DB 183 QIVRVDISINIQREWIPLPSHINTKGFAGADVKECIAFSSYICSPDPCFVLNHE 242
QY 359 IYCLSGNNTSACMSYKTEGALTTPYMTLKGSVIANCKMTTCRCADPPGIIISQNYGEAVSL 418
DB 359 IYCLSGNNTSACMSYKTEGALTTPYMTLKGSVIANCKMTTCRCADPPGIIISQNYGEAVSL 418
QY 243 MESCLSGNISQCPRTVVKSDIVPRYAFVNGGVVANCITTTCTGNGIGNRINQPPDQGVKI 302
DB 243 MESCLSGNISQCPRTVVKSDIVPRYAFVNGGVVANCITTTCTGNGIGNRINQPPDQGVKI 302
QY 419 IDQSCNVSLDGTITLRLSGEFDATYQKNSIQDSQVIVTGNLDISTELGNVNSISNAL 478
DB 419 IDQSCNVSLDGTITLRLSGEFDATYQKNSIQDSQVIVTGNLDISTELGNVNSISNAL 478
QY 303 ITHKECNTIGINGMLFNTNKEGTAFYTPNDITLNNVALDPIDISTELNKAKSDBEESK 362
DB 303 ITHKECNTIGINGMLFNTNKEGTAFYTPNDITLNNVALDPIDISTELNKAKSDBEESK 362
QY 479 DKLEESNKLKDVNVKLTSTLSALITYLVTLVSLVCGILSLVLACYLWKYKQAQKCTLLW 538
DB 479 DKLEESNKLKDVNVKLTSTLSALITYLVTLVSLVCGILSLVLACYLWKYKQAQKCTLLW 538
QY 363 EWTRSNQKLDISGNWQSSTIIIVLIMIIILFIINVTIIIAVKYRIQK----- 414
DB 363 EWTRSNQKLDISGNWQSSTIIIVLIMIIILFIINVTIIIAVKYRIQK----- 414
QY 539 LGNNTLDO 546
DB 539 LGNNTLDO 546
QY 415 --RNRVDQ 420
DB 415 --RNRVDQ 420

RESULT 14
US-10-371-264-6
; Sequence 6, Application US/10371264
; Publication No. US20030232061A1
; GENERAL INFORMATION:
; APPLICANT: Haller, Aurelia
; APPLICANT: Tang, Roderick
; TITLE OF INVENTION: RECOMBINANT PARAINFLUENZA VIRUS
; TITLE OF INVENTION: EXPRESSION SYSTEMS AND VACCINES
; TITLE OF INVENTION: COMBINING HETEROLOGOUS ANTIGENS
; TITLE OF INVENTION: DERIVED FROM METAPNEUMOVIRUS
; FILE REFERENCE: 7682-067-999
; CURRENT APPLICATION NUMBER: US/10/371,264
; CURRENT FILING DATE: 2003-02-21
; PRIOR APPLICATION NUMBER: 60/358,934
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 327
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 574
; TYPE: PRT
; ORGANISM: paramyxovirus
US-10-371-264-6

Query Match      7.7%; Score 211; DB 15; Length 574;
Best Local Similarity 20.4%; Pred. No. 3.1e-09;
Matches 111; Conservative 92; Mismatches 204; Indels 138; Gaps 21;

QY 47 DKAVNIVTSSQTSIGSIIVKLLPNMPKDKCAKAPLEAYNRTLTLLTPLGDSIRRIQESV 106
DB 47 DKAVNIVTSSQTSIGSIIVKLLPNMPKDKCAKAPLEAYNRTLTLLTPLGDSIRRIQESV 106

; STRANDEDNESS: <Unknown>
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 95:
US-10-267-748-95

Query Match      16.6%; Score 458; DB 12; Length 430;
Best Local Similarity 27.6%; Pred. No. 7.4e-31;
Matches 118; Conservative 81; Mismatches 219; Indels 10; Gaps 1;

QY 119 GAIIGGAALGVATAAQAIIAASAL-IAQANQANAIILRLKERIAATNEAV 178
DB 119 GAIIGGAALGVATAAQAIIAASAL-IAQANQANAIILRLKERIAATNEAV 178
QY 179 VGRNQFVNDQFNKTAQELDCIKITQQGVVGLNLYLTETLTVFGPQITSPALTIQAL 238
DB 179 VGRNQFVNDQFNKTAQELDCIKITQQGVVGLNLYLTETLTVFGPQITSPALTIQAL 238
QY 63 IKSQVQVYVKEIIVPSIARLGEAAAGLQGLIATLQHYSELINIFGDNIGSLQEKIGLQGI 122
DB 63 IKSQVQVYVKEIIVPSIARLGEAAAGLQGLIATLQHYSELINIFGDNIGSLQEKIGLQGI 122
QY 239 YNLAGNMDYLLTKLGVGNQSLSLGSLTGPNILYDSQTQLLGHIOVTLPSVGNLNM 298
DB 239 YNLAGNMDYLLTKLGVGNQSLSLGSLTGPNILYDSQTQLLGHIOVTLPSVGNLNM 298
QY 123 ASLYRTNITIFTTSTYDKYDIYDLFTBSIKVRVIDVDLNDYSITLQVRLPLRLTLNT 182
DB 123 ASLYRTNITIFTTSTYDKYDIYDLFTBSIKVRVIDVDLNDYSITLQVRLPLRLTLNT 182
QY 299 RATVLETLSVTTKGFASALVPKVMKGVSVIEBELDTSYCIETDLCTRIVTEPMSPG 358
DB 299 RATVLETLSVTTKGFASALVPKVMKGVSVIEBELDTSYCIETDLCTRIVTEPMSPG 358
QY 183 QIVRVDISINIQREWIPLPSHINTKGFAGADVKECIAFSSYICSPDPCFVLNHE 242
DB 183 QIVRVDISINIQREWIPLPSHINTKGFAGADVKECIAFSSYICSPDPCFVLNHE 242
QY 359 IYCLSGNNTSACMSYKTEGALTTPYMTLKGSVIANCKMTTCRCADPPGIIISQNYGEAVSL 418
DB 359 IYCLSGNNTSACMSYKTEGALTTPYMTLKGSVIANCKMTTCRCADPPGIIISQNYGEAVSL 418
QY 243 MESCLSGNISQCPRTVVKSDIVPRYAFVNGGVVANCITTTCTGNGIGNRINQPPDQGVKI 302
DB 243 MESCLSGNISQCPRTVVKSDIVPRYAFVNGGVVANCITTTCTGNGIGNRINQPPDQGVKI 302
QY 419 IDQSCNVSLDGTITLRLSGEFDATYQKNSIQDSQVIVTGNLDISTELGNVNSISNAL 478
DB 419 IDQSCNVSLDGTITLRLSGEFDATYQKNSIQDSQVIVTGNLDISTELGNVNSISNAL 478
QY 303 ITHKECNTIGINGMLFNTNKEGTAFYTPNDITLNNVALDPIDISTELNKAKSDBEESK 362
DB 303 ITHKECNTIGINGMLFNTNKEGTAFYTPNDITLNNVALDPIDISTELNKAKSDBEESK 362
QY 479 DKLEESNKLKDVNVKLTSTLSALITYLVTLVSLVCGILSLVLACYLWKYKQAQKCTLLW 538
DB 479 DKLEESNKLKDVNVKLTSTLSALITYLVTLVSLVCGILSLVLACYLWKYKQAQKCTLLW 538
QY 363 EWTRSNQKLDISGNWQSSTIIIVLIMIIILFIINVTIIIAVKYRIQK----- 414
DB 363 EWTRSNQKLDISGNWQSSTIIIVLIMIIILFIINVTIIIAVKYRIQK----- 414
QY 539 LGNNTLDO 546
DB 539 LGNNTLDO 546
QY 415 --RNRVDQ 420
DB 415 --RNRVDQ 420

RESULT 15
US-10-371-099-6
; Sequence 6, Application US/10371099
; Publication No. US20030232326A1
; GENERAL INFORMATION:
; APPLICANT: Haller, Aurelia
; APPLICANT: Tang, Roderick
; APPLICANT: Fouchier, Roderick
; APPLICANT: Van Den Hoogen, Bernadetta
; APPLICANT: Osterhaus, Albertus
; TITLE OF INVENTION: METAPNEUMOVIRUS STRAINS AND THEIR
; TITLE OF INVENTION: USE IN VACCINE FORMULATIONS AND AS
; TITLE OF INVENTION: VECTORS FOR EXPRESSION OF
; TITLE OF INVENTION: ANTIGENIC SEQUENCES
; FILE REFERENCE: 7682-063-999
; CURRENT APPLICATION NUMBER: US/10/371,099
; CURRENT FILING DATE: 2003-02-21
; NUMBER OF SEQ ID NOS: 389
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 574
; TYPE: PRT
; ORGANISM: paramyxovirus
; FEATURE:
; OTHER INFORMATION: paramyxovirus F protein hRSV B
US-10-371-099-6

Query Match      7.7%; Score 211; DB 15; Length 574;
Best Local Similarity 20.4%; Pred. No. 3.1e-09;
Matches 111; Conservative 92; Mismatches 204; Indels 138; Gaps 21;

QY 47 DKAVNIVTSSQTSIGSIIVKLLPNMPKDKCAKAPLEAYNRTLTLLTPLGDSIRRIQESV 106
DB 47 DKAVNIVTSSQTSIGSIIVKLLPNMPKDKCAKAPLEAYNRTLTLLTPLGDSIRRIQESV 106

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OM protein - protein search, using sw model

Run on: April 17, 2004, 06:54:07 ; Search time 97 Seconds
(without alignments)
1610.812 Million cell updates/sec

Title: US-10-725-841-2

Perfect score: 2757
Sequence: 1 MGRSSTRIPVPLMLTVRA.....KTLMLGNNTDQMRATMM 553

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_29Jan04:*

1: Geneseq19808:*

2: Geneseq19908:*

3: Geneseq20008:*

4: Geneseq20018:*

5: Geneseq20028:*

6: Geneseq20038:*

7: Geneseq20038:*

8: Geneseq20048:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2724	98.8	553	2 AAR10065	Aar10065 Newcastle
2	2716	98.5	553	6 ABR56236	Abr56236 Newcastle
3	2620	95.0	1103	6 ABR39678	Abr39678 Amino aci
4	2616	94.9	553	3 AAY51231	Aay51231 Newcastle
5	2610	94.7	553	2 AAR58858	Aar58858 Newcastle
6	2610	94.7	553	2 AAR49141	Aar49141 Newcastle
7	2610	94.7	553	2 AAW06828	Aaw06828 Newcastle
8	2610	94.7	553	2 AAR10691	Aar10691 Newcastle
9	2610	94.7	553	2 AAY21983	Aay21983 Seq ID No
10	2610	94.7	553	3 AAB36039	Aab36039 Protein e
11	2606	94.7	553	2 AAR14480	Aar14480 Newcastle
12	2606	94.5	553	2 AAW44941	Aaw44941 Newcastle
13	2606	94.5	553	1 AAP70176	Aap70176 Sequence
14	2603	94.4	553	1 AAB31709	Aab31709 Newcastle
15	2493.5	90.4	564	5 AAG31709	Aag31709 Newcastle
16	2401	87.1	526	1 AAP80986	Aap80986 Sequence
17	2386	86.5	526	2 AAR20501	Aar20501 Newcastle
18	2086.5	75.7	436	6 ABO10250	Abo10250 Newcastle
19	2065	74.9	437	4 AAU14030	Aau14030 Peptide s
20	717	26.0	529	6 ABJ18515	Abj18515 Human Cry
21	715	25.9	529	6 ABJ18516	Abj18516 Canine pa
22	714	25.9	551	6 ABJ18506	Abj18506 Human Cry
23	712	25.8	551	6 ABJ18514	Abj18514 Simian vi
24	707	25.6	551	6 ABJ18513	Abj18513 Simian vi
25	706	25.6	529	4 ABP98712	Abp98712 Canine pa

26	696.5	25.3	532	6	ABJ18507	Human Cry
27	694.5	25.2	538	4	ABR67476	Abr67476 Amino aci
28	689	25.0	542	2	AAR24076	Aar24076 Para-infl
29	623.5	22.6	662	2	AAR83304	Aar83304 Canine di
30	623.5	22.6	662	5	AAW47653	Aaw47653 Canine di
31	621.5	22.5	662	3	ABO8102	Abo8102 Amino aci
32	621.5	22.5	662	4	AAW50124	Aaw50124 Canine di
33	610.5	22.1	550	4	AAR42394	Aar42394 Moraten h
34	610.5	22.1	550	4	AAW73722	Aaw73722 Measles v
35	608.5	22.1	550	2	AAR34540	Aar34540 F protein
36	606.5	22.0	550	2	AAW42396	Aaw42396 Chicago 1
37	606.5	22.0	550	2	AAW42397	Aaw42397 Consensus
38	606.5	22.0	550	2	AAW42395	Aaw42395 San Diego
39	605.5	22.0	550	2	AAW94759	Aaw94759 Mutant me
40	605.5	22.0	550	4	AAW73721	Aaw73721 Measles v
41	602.5	21.9	550	2	AAW94760	Aaw94760 Mutant me
42	590.5	21.4	449	6	ABJ18509	Abj18509 Human Cry
43	552	20.0	539	2	ABR39283	Abr39283 Parainflu
44	534	19.4	438	6	ABO10249	Abo10249 Canine di
45	522.5	19.0	439	4	AAU14029	Aau14029 Peptide s

ALIGNMENTS

RESULT 1
AAR10065
ID AAR10065 standard; protein; 553 AA.
XX
AC AAR10065;
XX
XX
DT 25-MAR-2003 (revised)
DT 14-MAR-1991 (first entry)
XX
XX
DE Newcastle disease virus (NDV) F gene product.
XX
KW Avipoxvirus; fowlpoxvirus; vaccine.
XX
OS Newcastle disease virus.
XX
PN EP404576-A.
XX
PD 27-DEC-1990.
XX
PF 21-JUN-1990; 90EP-00306806.
XX
PR 22-JUN-1989; 89JP-00160157.
XX
XX (JAPG) NIPPON ZEON KK.
PA (SHIO) SHIONOGI & CO LTD.
PA (YANA/) YANAGIDA N.
XX
PI Yangida N, Saeki S, Okawa S, Kmanogawa K, Iritani Y, Sawaguchi K;
XX WPI: 1991-001591/01.
DR N-PSDB; AAQ10060.
DR
XX
XX
PT Recombinant avipox virus - contg. CDNA coding for Newcastle disease virus
in region non-essential for proliferation, used as live vaccine in fowls.
PT
XX
XX Claim 3; Fig 3; 23pp; English.
XX
XX The sequence encoding the protein may be incorporated into a recombinant
CC Avipoxvirus and used as a live vaccine in fowls, providing immunity to
CC fowlpoxvirus and NDV. (Updated on 25-MAR-2003 to correct PA field.)
XX
SQ Sequence 553 AA;

Query Match 98.8%; Score 2724; DB 2; Length 553;
Best Local Similarity 98.4%; Pred. No. 9.8e-226;
Matches 544; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

QY 1 MGRSSTRIPVPLMLTVRAALSCVPTSSLDGRPLAAGIVVTGDKAVNIYTSQTGS 60

```

Db      1 MGRSRSTRIPVPLMLTVRVALALSCVPTSSLDGRPLAAAGIVVTGDKAVNIYTSQTGS 60
QY      61 IIVKLLPNMPKDEACAKAPLEAYNRITLTLLTPLGDSIRRIQESVTTSGGKQGRILGA 120
Db      61 IIVKLLPNMPKDEACAKAPLEAYNRITLTLLTPLGDSIRRIQESVTTSGGKQGRILGA 120
QY      121 IIGGAALGVATAAQITAAASALIQANQANILRLKESIAATNEAVHEVTGSLQAVAG 180
Db      121 IIGGAALGVATAAQITAAASALIQANQANILRLKESIAATNEAVHEVTGSLQAVAG 180
QY      181 KMQQFVNDQFNKTAQELDCIKITQOVGVNELNLYLTETTVFGPQITSPALTIQALYN 240
Db      181 KMQQFVNDQFNKTAQELDCIKITQOVGVNELNLYLTETTVFGPQITSPALTIQALYN 240
QY      241 LAGNNMDYLLTKLGVGNQLSSLTGSLITGNPILYDSOTQLLGIQVTLPSVGNLNMRA 300
Db      241 LAGNNMDYLLTKLGVGNQLSSLTGSLITGNPILYDSOTQLLGIQVTLPSVGNLNMRA 300
QY      301 TYLETLSVSTTKGFASALVPKVMKGVSVIEELDTSCYIETDLDLYCTRIVTFPMSPGIY 360
Db      301 TYLETLSVSTTKGFASALVPKVMKGVSVIEELDTSCYIETDLDLYCTRIVTFPMSPGIY 360
QY      361 SCLSGNTSACWYSKTEGALTTPYMTLKGSVIANCKMTTCRCADPPGIISQNYGEAVSLID 420
Db      361 SCLSGNTSACWYSKTEGALTTPYMTLKGSVIANCKMTTCRCADPPGIISQNYGEAVSLID 420
QY      421 RQSCNVLSLDGITRLSGEFDATYQKNISIQDSQVIVTGNLDISTELGNVNNISNALDK 480
Db      421 RQSCNVLSLDGITRLSGEFDATYQKNISIQDSQVIVTGNLDISTELGNVNNISNALDK 480
QY      481 LEESNSKLDKVNKLTSTSAITYIVLTIVLSVCGILSLVACVLMYKQKAAQKTLWL 540
Db      481 LEESNSKLDKVNKLTSTSAITYIVLTIVLSVCGILSLVACVLMYKQKAAQKTLWL 540
QY      541 NNTLDQMRATTKM 553
Db      541 NNTLDQMRATTKM 553

```

RESULT 2

ABR56236
ID ABR56236 standard; protein; 553 AA.

XX
AC ABR56236;

XX
DT 20-NOV-2003 (first entry)

XX
DE Newcastle disease virus (NDV) Fusion (F)-protein.

XX
KW F-protein; virucide; vaccine; anti-viral; Fusion protein;

XX
KW protein co-ordinate data.

XX
OS Newcastle disease virus.

XX
PN WO2003040178-A1.

XX
PD 15-MAY-2003.

XX
PF 08-NOV-2002; 2002WO-AU001522.

XX
PR 09-NOV-2001; 2001AU-00008784.

XX
PA (BIOT-) BIOTA HOLDINGS LTD.

XX
PI Morton CJ, Parker MW, Ryan J;

XX
DR WPI; 2003-441524/41.

XX
XX Identifying, screening or modifying anti-viral agents, by generating a 3-
PT dimensional structure model of respiratory Syncytial virus-F protein
PT having a target site to interact with an anti-viral agent that inhibit
PT RSV-F.

XX

PS Disclosure; Fig 1; 224pp; English.

XX

CC The present invention relates to a method (M1) for identifying a
CC candidate anti-viral agent (I), screening compounds and/or chemical
CC complexes for (I), modifying (I) to improve anti-viral activity, or
CC producing anti-viral agents, by generating a 3-dimensional structure
CC model of Respiratory Syncytial virus (RSV) Fusion (F)-protein with 3-
CC dimensional structure of target site to which an anti-viral agent may
CC interact and thus inhibit RSV-F protein activity. The present sequence is
CC the Newcastle Disease Virus (NDV) F-protein used in a sequence alignment
CC with the RSV F-protein sequence (ABR56234)

XX SQ Sequence 553 AA;

Query Match 98.5%; Score 2716; DB 6; Length 553;

Best Local Similarity 98.2%; Pred. No. 4.8e-225;

Matches 543; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

QY 1 MGRSRSTRIPVPLMLTVRVALALSCVPTSSLDGRPLAAAGIVVTGDKAVNIYTSQTGS 60

Db 1 MGRSRSTRIPVPLMLTVRVALALSCVPTSSLDGRPLAAAGIVVTGDKAVNIYTSQTGS 60

QY 61 IIVKLLPNMPKDEACAKAPLEAYNRITLTLLTPLGDSIRRIQESVTTSGGKQGRILGA 120

Db 61 IIVKLLPNMPKDEACAKAPLEAYNRITLTLLTPLGDSIRRIQESVTTSGGKQGRILGA 120

QY 121 IIGGAALGVATAAQITAAASALIQANQANILRLKESIAATNEAVHEVTGSLQAVAG 180

Db 121 IIGGAALGVATAAQITAAASALIQANQANILRLKESIAATNEAVHEVTGSLQAVAG 180

QY 181 KMQQFVNDQFNKTAQELDCIKITQOVGVNELNLYLTETTVFGPQITSPALTIQALYN 240

Db 181 KMQQFVNDQFNKTAQELDCIKITQOVGVNELNLYLTETTVFGPQITSPALTIQALYN 240

QY 241 LAGNNMDYLLTKLGVGNQLSSLTGSLITGNPILYDSOTQLLGIQVTLPSVGNLNMRA 300

Db 241 LAGNNMDYLLTKLGVGNQLSSLTGSLITGNPILYDSOTQLLGIQVTLPSVGNLNMRA 300

QY 301 TYLETLSVSTTKGFASALVPKVMKGVSVIEELDTSCYIETDLDLYCTRIVTFPMSPGIY 360

Db 301 TYLETLSVSTTKGFASALVPKVMKGVSVIEELDTSCYIETDLDLYCTRIVTFPMSPGIY 360

QY 361 SCLSGNTSACWYSKTEGALTTPYMTLKGSVIANCKMTTCRCADPPGIISQNYGEAVSLID 420

Db 361 SCLSGNTSACWYSKTEGALTTPYMTLKGSVIANCKMTTCRCADPPGIISQNYGEAVSLID 420

QY 421 RQSCNVLSLDGITRLSGEFDATYQKNISIQDSQVIVTGNLDISTELGNVNNISNALDK 480

Db 421 RQSCNVLSLDGITRLSGEFDATYQKNISIQDSQVIVTGNLDISTELGNVNNISNALDK 480

QY 481 LEESNSKLDKVNKLTSTSAITYIVLTIVLSVCGILSLVACVLMYKQKAAQKTLWL 540

Db 481 LEESNSKLDKVNKLTSTSAITYIVLTIVLSVCGILSLVACVLMYKQKAAQKTLWL 540

QY 541 NNTLDQMRATTKM 553

Db 541 NNTLDQMRATTKM 553

RESULT 3

ABR39678

ID ABR39678 standard; protein; 1103 AA.

XX
AC ABR39678;

XX
DT 23-JUN-2003 (first entry)

XX
DE Amino acid sequence of F protein and partial HN protein.

XX
KW NDV; lentogenic; oncolytic; fusion glycoprotein; F gene; HN gene;

XX
KW haemagglutinin-neuraminidase; cytostatic; gene therapy; cancer.

181 KMQQFVNDQFNKTAQELDCIKITQOVGVNELNLYLTETTTVPQITSPALQTQIALYN 240
181 KMQQFVNDQFNKTAQELDCIKITQOVGVNELNLYLTETTTVPQITSPALQTQIALYN 240
241 LAGGNDYLLTKLGVGNQSLIGSLITGNPILYDSQTQLLGIQVTLPSVGNLNNMRA 300
241 LAGGNDYLLTKLGVGNQSLIGSLITGNPILYDSQTQLLGIQVTLPSVGNLNNMRA 300
301 TYLETLSVSTTKGFASALVPKVMKGVSVIEELDTSYCIETDLDLYCTRIIVTFPMSPGIY 360
301 TYLETLSVSTTKGFASALVPKVMKGVSVIEELDTSYCIETDLDLYCTRIIVTFPMSPGIY 360
361 SCLSGNTSACMYSKTEGALTTPYMTLKGSVIANCKMTTCRCADPPGIIISQNYGEAVSLID 420
361 SCLSGNTSACMYSKTEGALTTPYMTLKGSVIANCKMTTCRCADPPGIIISQNYGEAVSLID 420
421 RQSCNVLSLDGITLRLSGEFDATYQKNISIQDSQVIVTGNLIDISTELGNVNSISNALDK 480
421 RQSCNVLSLDGITLRLSGEFDATYQKNISIQDSQVIVTGNLIDISTELGNVNSISNALDK 480
481 LEESNSKLDKVNKLTSTLSALITVIVTSLVCGILSLVACLYMYKQKAAQKTLMLG 540
481 LEESNSKLDKVNKLTSTLSALITVIVTSLVCGILSLVACLYMYKQKAAQKTLMLG 540
541 NNTLDQMRATTKM 553
541 NNTLDQMRATTKM 553

RESULT 2

A46329
cell fusion glycoprotein precursor - Newcastle disease virus (strain D26/76)
N;Contains: fusion glycoprotein F1; fusion glycoprotein F2
C;Species: Newcastle disease virus
C;Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 16-Jul-1999
C;Accession: A46329
R;Royoda, T.; Sakaguchi, T.; Hirota, H.; Gotoh, B.; Kuma, K.; Miyata, T.; Nagai, Y.
Virology 169, 273-282, 1989
A;Title: Newcastle disease virus evolution. II. Lack of gene recombination in generating
A;Reference number: A46329; MUID:89204898; PMID:2705298
A;Accession: A46329
A;Molecule type: genomic RNA
A;Residues: 1-553 <TOY>
A;Cross-references: GB:M24692; NID:g293919; PIDN:AAA46643.1; PID:g293920
C;Genetics:
A;Gene: F

C;Superfamily: parainfluenza virus cell fusion protein
C;Keywords: Glycoprotein; membrane fusion; transmembrane protein
F;1-25/Domain: signal sequence #status predicted <SIG>
F;26-117/Product: cell fusion glycoprotein F2 #status predicted <FF2>
F;118-553/Product: cell fusion glycoprotein F1 #status predicted <FF1>
F;495-528/Domain: transmembrane #status predicted <TMN>
F;85,191,366,447,471/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 98.8%; Score 2724; DB 1; Length 553;
Best Local Similarity 98.4%; Pred. No. 1.4e-162;
Matches 544; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

1 MGSRSSTRIPVPLMLTVRVALALSCVPTSSLDGRPLAAGIVTGDKAVNIYTSSQTGS 60
1 MGSRSSTRIPVPLMLTVRIMALSCVPTSSLDGRPLAAGIVTGDKAVNIYTSSQTGS 60
61 IIVKLLPNMPKDEACAKAPLEAYNRTLTLLTPLGDSIRRIQESVTTSGGKQGRLLGA 120
61 IIVKLLPNMPKDEACAKAPLEAYNRTLTLLTPLGDSIRRIQESVTTSGGKQGRLLGA 120
121 IIGGALGVATAAQITAAASALIOANQNAANILRLKERIAATNEAVHEVTDGLSOLAVAG 180
121 IIGGALGVATAAQITAAASALIOANQNAANILRLKERIAATNEAVHEVTDGLSOLAVAG 180
181 KMQQFVNDQFNKTAQELDCIKITQOVGVNELNLYLTETTTVPQITSPALQTQIALYN 240
181 KMQQFVNDQFNKTAQELDCIKITQOVGVNELNLYLTETTTVPQITSPALQTQIALYN 240

241 LAGGNDYLLTKLGVGNQSLIGSLITGNPILYDSQTQLLGIQVTLPSVGNLNNMRA 300
241 LAGGNDYLLTKLGVGNQSLIGSLITGNPILYDSQTQLLGIQVTLPSVGNLNNMRA 300
301 TYLETLSVSTTKGFASALVPKVMKGVSVIEELDTSYCIETDLDLYCTRIIVTFPMSPGIY 360
301 TYLETLSVSTTKGFASALVPKVMKGVSVIEELDTSYCIETDLDLYCTRIIVTFPMSPGIY 360
361 SCLSGNTSACMYSKTEGALTTPYMTLKGSVIANCKMTTCRCADPPGIIISQNYGEAVSLID 420
361 SCLSGNTSACMYSKTEGALTTPYMTLKGSVIANCKMTTCRCADPPGIIISQNYGEAVSLID 420
421 RQSCNVLSLDGITLRLSGEFDATYQKNISIQDSQVIVTGNLIDISTELGNVNSISNALDK 480
421 RQSCNVLSLDGITLRLSGEFDATYQKNISIQDSQVIVTGNLIDISTELGNVNSISNALDK 480
481 LEESNSKLDKVNKLTSTLSALITVIVTSLVCGILSLVACLYMYKQKAAQKTLMLG 540
481 LEESNSKLDKVNKLTSTLSALITVIVTSLVCGILSLVACLYMYKQKAAQKTLMLG 540
541 NNTLDQMRATTKM 553
541 NNTLDQMRATTKM 553

RESULT 3

S23621
gene F protein - Newcastle disease virus
C;Species: Newcastle disease virus
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 25-Oct-1996
C;Accession: S23621
R;Pritzer, E.; Kuroda, K.; Garten, W.; Nagai, Y.; Klenk, H.D.
Virus Res. 15, 237-242, 1990
A;Title: A host range mutant of Newcastle disease virus with an altered cleavage site f
A;Reference number: S23620; MUID:90261333; PMID:2188464
A;Accession: S23621
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-553 <PRI>
A;Cross-references: EMBL:Z12110
C;Superfamily: parainfluenza virus cell fusion protein

Query Match 97.6%; Score 2691; DB 2; Length 553;
Best Local Similarity 98.2%; Pred. No. 1.7e-160;
Matches 543; Conservative 1; Mismatches 9; Indels 0; Gaps 0;

1 MGSRSSTRIPVPLMLTVRVALALSCVPTSSLDGRPLAAGIVTGDKAVNIYTSSQTGS 60
1 MGSRSSTRIPVPLMLTVRVALALSCVPTSSLDGRPLAAGIVTGDKAVNIYTSSQTGS 60
61 IIVKLLPNMPKDEACAKAPLEAYNRTLTLLTPLGDSIRRIQESVTTSGGKQGRLLGA 120
61 IIVKLLPNMPKDEACAKAPLEAYNRTLTLLTPLGDSIRRIQESVTTSGGKQGRLLGA 120
121 IIGGALGVATAAQITAAASALIOANQNAANILRLKERIAATNEAVHEVTDGLSOLAVAG 180
121 IIGGALGVATAAQITAAASALIOANQNAANILRLKERIAATNEAVHEVTDGLSOLAVAG 180
181 KMQQFVNDQFNKTAQELDCIKITQOVGVNELNLYLTETTTVPQITSPALQTQIALYN 240
181 KMQQFVNDQFNKTAQELDCIKITQOVGVNELNLYLTETTTVPQITSPALQTQIALYN 240
241 LAGGNDYLLTKLGVGNQSLIGSLITGNPILYDSQTQLLGIQVTLPSVGNLNNMRA 300
241 LAGGNDYLLTKLGVGNQSLIGSLITGNPILYDSQTQLLGIQVTLPSVGNLNNMRA 300
301 TYLETLSVSTTKGFASALVPKVMKGVSVIEELDTSYCIETDLDLYCTRIIVTFPMSPGIY 360
301 TYLETLSVSTTKGFASALVPKVMKGVSVIEELDTSYCIETDLDLYCTRIIVTFPMSPGIY 360
361 SCLSGNTSACMYSKTEGALTTPYMTLKGSVIANCKMTTCRCADPPGIIISQNYGEAVSLID 420
361 SCLSGNTSACMYSKTEGALTTPYMTLKGSVIANCKMTTCRCADPPGIIISQNYGEAVSLID 420

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: April 18, 2004, 01:19:18 ; Search time 46 Seconds
(without alignments)
1156.389 Million cell updates/sec

Title: US-10-725-841-2
Perfect score: 2757
Sequence: 1 MGRSRSTRIPVPLMLTVRVA.....KTLMLGNNTLDQMRATTHM 553

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues 283366
Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 78:*
1: Pir1:*
2: Pir2:*
3: Pir3:*
4: Pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2724	98.8	553	1 VGNZU1	cell fusion glycop
2	2724	98.8	553	1 A46329	cell fusion glycop
3	2691	97.6	553	2 S23621	gene F protein - N
4	2684	97.4	553	1 B46329	cell fusion glycop
5	2658	96.4	553	2 S38785	gene F protein - N
6	2625	95.2	553	1 H46329	cell fusion glycop
7	2622	95.1	553	1 D46329	cell fusion glycop
8	2606	94.5	553	1 VGNZTE	cell fusion glycop
9	2603	94.4	553	1 VGNZNV	cell fusion glycop
10	2602	94.4	553	2 S40163	cell fusion glycop
11	2599	94.3	553	2 S06345	cell fusion glycop
12	2598	94.2	553	1 A36830	cell fusion glycop
13	2593	94.1	553	1 G46329	cell fusion glycop
14	2592	94.0	553	1 B36830	cell fusion glycop
15	2589	93.9	553	1 VGNZGB	cell fusion glycop
16	2588	93.9	553	1 E46329	cell fusion glycop
17	2585	93.8	553	1 I46329	cell fusion glycop
18	2579	93.5	553	1 VGNZND	cell fusion glycop
19	2575	93.4	553	2 S38784	gene F protein - N
20	2555	92.7	553	2 S23622	gene F protein - N
21	2554	92.6	553	2 S23620	F protein - Newcas
22	2549	92.5	553	2 S38786	gene F protein - N
23	1018.5	36.9	534	2 A37483	F protein - Muraya
24	717	26.0	529	1 VGNZSP	cell fusion glycop
25	712.5	25.8	538	1 VGNZNM	cell fusion glycop
26	712.5	25.8	538	2 S52472	cell fusion protei
27	704	25.5	538	1 VGNZMS	cell fusion glycop
28	704	25.5	531	1 VGNZFP	cell fusion glycop
29	701.5	25.4	538	1 VGNZMU	cell fusion glycop

ALIGNMENTS

RESULT 1

VGNZU1

cell fusion glycoprotein precursor - Newcastle disease virus (strains Ulster and ULS/6 N; Contains: fusion glycoprotein F1; fusion glycoprotein F2

C; Species: Newcastle disease virus

C; Date: 30-Jun-1989 #sequence_revision 30-Jun-1989 #text_change 16-Jun-2000

C; Accession: A29823, C46329

R; Millar, N.S.; Chambers, P.; Emerson, P.T.

J. Gen. Virol. 69, 613-620, 1988

A; Title: Nucleotide sequence of the fusion and haemagglutinin-neuraminidase glycoprote

ns.

A; Reference number: A92799; MUID:88171450; PMID:3351479

A; Accession: A29823

A; Molecule type: mRNA

A; Residues: 1-553 <ML>

A; Cross-references: GB:D00243; NID:G222174; PIDN:BAA00173.1; PID:G222175

A; Experimental source: strain Ulster

R; Toyoda, T.; Sakaguchi, T.; Hirota, H.; Gotoh, B.; Kuma, K.; Miyata, T.; Nagai, Y.

Virol. 169, 273-282, 1989

A; Title: Newcastle disease virus evolution. II. Lack of gene recombination in generati

A; Reference number: A46329; MUID:89204898; PMID:2705298

A; Accession: C46329

A; Molecule type: genomic RNA

A; Residues: 1-553 <TOY>

A; Cross-references: GB:M24694; NID:G293923; PIDN:AAA46645.1; PID:G293924

A; Experimental source: strain ULS/67

C; Genetics:

A; Gene: F

C; Superfamily: parainfluenza virus cell fusion protein

C; Keywords: glycoprotein; membrane fusion; transmembrane protein

F; 1-25/Domain: signal sequence #status predicted <SIG>

F; 26-117/Product: cell fusion glycoprotein F2 #status predicted <FP2>

F; 118-553/Product: cell fusion glycoprotein F1 #status predicted <FP1>

F; 495-528/Domain: transmembrane #status predicted <TM>

F; 85,191,366,447,471/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 98.8%; Score 2724; DB 1; Length 553;

Best Local Similarity 99.1%; Pred. No. 1.4e-162;

Matches 548; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 MGRSRSTRIPVPLMLTVRVALSCVCTSSSLDGRPLAAAGIVVTGDKAVNIYTSQTGS 60

|||||

Db 1 MGRSRSTRIPVPLMLTVRVALSCVCTSSSLDGRPLAAAGIVVTGDKAVNIYTSQTGS 60

|||||

QY 61 IIVKLLPNMPKDEACAKAPLEAYNRTLTLLPLGDSIRRIQESVTTSGGKGRLLGA 120

|||||

Db 61 IIVKLLPNMPKDEACAKAPLEAYNRTLTLLPLGDSIRRIQESVTTSGGKGRLLGA 120

|||||

QY 121 IIGGALGVATAAQITAAASALIQANQNAANILRLK AATNEAVHEVTDGLSQLAVAG 180

|||||

Db 121 IIGGALGVATAAQITAAASALIQANQNAANILRLK AATNEAVHEVTDGLSQLAVAG 180

|||||

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OM protein - protein search, using sw model

Run on: April 17, 2004, 06:54:07 ; Search time 40 Seconds
(without alignments)
719.870 Million cell updates/sec

Title: US-10-725-841-2

Perfect score: 2757

Sequence: 1 MGRSRSTRIPVPLMLTVRA.....KILLWLGNTLDQMRATYKN 553

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_42.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2724	98.8	553	1	VGLF_NDND
2	2724	98.8	553	1	VGLF_NDVU
3	2684	97.4	553	1	VGLF_NDVQ
4	2622	95.1	553	1	VGLF_NDVH4
5	2618	95.0	553	1	VGLF_NDVA
6	2606	94.5	553	1	VGLF_NDVT
7	2603	94.4	553	1	VGLF_NDVB
8	2598	94.2	553	1	VGLF_NDVH3
9	2593	94.1	553	1	VGLF_NDVGT
10	2588	93.9	553	1	VGLF_NDVL
11	2588	93.9	553	1	VGLF_NDVL
12	2579	93.5	553	1	VGLF_NDVM
13	717	26.0	529	1	VGLF_SV5
14	712.5	25.8	538	1	VGLF_MMPM
15	706	25.6	551	1	VGLF_P12H
16	704	25.5	538	1	VGLF_MMP1
17	704	25.5	551	1	VGLF_P12HT
18	701.5	25.4	538	1	VGLF_MMPR
19	701	25.4	551	1	VGLF_P12HG
20	691	25.1	538	1	VGLF_MMP5
21	691	25.1	538	1	VGLF_MMP5
22	636	23.1	631	1	VGLF_P12H
23	631	22.9	546	1	VGLF_P12H
24	621.5	22.5	662	1	VGLF_CDOV
25	610.5	22.1	550	1	VGLF_MEAS
26	608.5	22.1	546	1	VGLF_RINDL
27	605.5	22.0	550	1	VGLF_MEAS
28	603.5	21.9	546	1	VGLF_RINDK
29	599.5	21.7	546	1	VGLF_RINDR
30	590.5	21.4	534	1	VGLF_MEAS
31	581.5	21.1	529	1	VGLF_MEAS
32	546.5	19.8	539	1	VGLF_P13H4
33	521	18.9	565	1	VGLF_SENDJ

34 515 18.7 565 1 VGLF_SENDF
35 512 18.6 540 1 VGLF_P13B
36 511 18.5 565 1 VGLF_SENDZ
37 497.5 18.0 555 1 VGLF_P11HC
38 497 18.0 565 1 VGLF_SENDH
39 214 7.8 574 1 VGLF_HRSV1
40 203 7.4 574 1 VGLF_HRSVA
41 201 7.3 574 1 VGLF_HRSVR
42 199 7.2 574 1 VGLF_HRSVL
43 198 7.2 574 1 VGLF_HRSVR
44 194 7.0 538 1 VGLF_TRTV
45 193 7.0 572 1 VGLF_BRSVA

P12575 sendai viru
P09990 bovine para
P04855 sendai viru
P12605 human para
P04856 sendai viru
P13843 human respi
P03420 human respi
P11209 human respi
P12568 human respi
P23728 bovine respi
P24614 turkey rhin
P29791 bovine resp

ALIGNMENTS

RESULT 1
VGLF_NDND
ID VGLF_NDND STANDARD; PRT; 553 AA.
AC P35936;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Fusion glycoprotein precursor [Contains: Fusion glycoprotein F2;
DE Fusion glycoprotein F1].
GN F.
OS Newcastle disease virus (strain D25/76) (NDV).
OC Viruses; ssRNA negative-strand viruses; Mononegavirales;
OC Paramyxoviridae; Paramyxovirinae; Rubulavirus.
OX NCBI_TaxID=11180;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=89204998; PubMed=2705238;
RA Toyoda T., Sakaguchi T., Hirota H., Gotoh B., Kuma K., Miyata T.,
RA Nagai Y.;
RT "Newcastle disease virus evolution. II. Lack of gene recombination in
RT generating virulent and avirulent strains.";
RL Virology 169:273-282(1989).
CC -!- FUNCTION: This protein directs fusion of viral and cellular
CC membranes.
CC -!- SUBUNIT: THE MATURE FORM IS A DIMER OF POLYPEPTIDES F-1 AND F-2
CC LINKED BY A DISULFIDE BOND.
CC -!- SIMILARITY: Belongs to the paramyxoviruses fusion glycoprotein
CC family.
CC
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CC
CC EMBL; M24692; AAA46643.1; -
CC PIR; A46329; A46329.
CC PDB; 1G5G; 27-FEB-02.
CC InterPro; IPR000776; Fusion gly.
CC Pfam; PF00523; fusion_gly; 1.
KW Glycoprotein; Fusion protein; Transmembrane; Envelope protein; Signal;
KW Lipoprotein; Palmitate; 3D-structure.
FT SIGNAL 1 25
FT CHAIN 26 553 FUSION GLYCOPROTEIN FO.
FT CHAIN 26 116 F2 PROTEIN.
FT CHAIN 117 553 F1 PROTEIN.
FT TRANSMEM 117 136 POTENTIAL.
FT DOMAIN 137 500 EXTRACELLULAR.
FT TRANSMEM 501 527 POTENTIAL.
FT DOMAIN 528 553 CYTOPLASMIC.
FT TRANSMEM 85 85 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 191 191 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 366 366 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 447 447 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 471 471 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT LIPID 523 523 S-palmitoyl cysteine (in host)
 SQ SEQUENCE 553 AA; 58892 MW; B90AA98D77CCC470 CRC64;
 Query Match 98.8%; Score 2724; DB 1; Length 553;
 Best Local Similarity 98.4%; Pred. No. 2.5e-162;
 Matches 544; Conservative 4; Mismatches 5; Indels 0; Gaps 0;
 QY 1 MGRSSSTRIPVPLMLTVRVALALSCVPTSSLDGRPLAAAGIVVTGKAVNIYTSQTGS 60
 DB 1 MGRSSSTRIPVPLMLTVRVALALSCVPTSSLDGRPLAAAGIVVTGKAVNIYTSQTGS 60
 QY 61 IIVKLLNMPKDEKACAKAPLEAYNRTLTLLTFLGDSIRRIQSVTSSGGKQRLIGA 120
 DB 61 IIVKLLNMPKDEKACAKAPLEAYNRTLTLLTFLGDSIRRIQSVTSSGGKQRLIGA 120
 QY 121 IIGGAALGVATAAQTAAALIQANQNAANILRLKERIAATNEAVHEVTDGLSOLAVAVG 180
 DB 121 IIGGAALGVATAAQTAAALIQANQNAANILRLKERIAATNEAVHEVTDGLSOLAVAVG 180
 QY 181 KMQQFVNDQFNKTAQELDCIKITQOVGVNELMLYLTELTTVFGPQITSPALTIQALYN 240
 DB 181 KMQQFVNDQFNKTAQELDCIKITQOVGVNELMLYLTELTTVFGPQITSPALTIQALYN 240
 QY 241 LAGNMDYLLTKLGVGNQLSSGLITGNPILYDSQTOLLGIQVTLPSVGNLNNMRA 300
 DB 241 LAGNMDYLLTKLGVGNQLSSGLITGNPILYDSQTOLLGIQVTLPSVGNLNNMRA 300
 QY 301 TYLETSLVSTTKGFASALVPKVMKGVSVIEELDTSYCIETDLDLYCTRIVTFPMSPGIY 360
 DB 301 TYLETSLVSTTKGFASALVPKVMKGVSVIEELDTSYCIETDLDLYCTRIVTFPMSPGIY 360
 QY 361 SCLSGNTSACMYSTEGALTPYMTLKGSVIANCKMTTCRCADPPGIISQNYGEAVSLID 420
 DB 361 SCLSGNTSACMYSTEGALTPYMTLKGSVIANCKMTTCRCADPPGIISQNYGEAVSLID 420
 QY 421 ROSCNVLSDGTLRLSGEPDATYOKNISIDSOVIVTGNLDISTELGNVNNISNALDK 480
 DB 421 ROSCNVLSDGTLRLSGEPDATYOKNISIDSOVIVTGNLDISTELGNVNNISNALDK 480
 QY 481 LEESNKLKDNVNLKTSALITYIVLTIVSLVCGILSLVLAICYLMYKQAKQKTLMLWG 540
 DB 481 LEESNKLKDNVNLKTSALITYIVLTIVSLVCGILSLVLAICYLMYKQAKQKTLMLWG 540
 QY 541 NNTLDQMRATTKM 553
 DB 541 NNTLDQMRATTKM 553

RESULT 2

VCLF_NDVU STANDARD; PRT; 553 AA.
 ID VCLF_NDVU STANDARD; PRT; 553 AA.
 AC P12570;
 DT 01-OCT-1989 (Rel. 12, Created)
 DT 01-OCT-1989 (Rel. 12, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Fusion glycoprotein precursor [Contains: Fusion glycoprotein F2;
 DE Fusion glycoprotein F1].
 GN F.
 OS Newcastle disease virus (strain Ulster/67) (NDV).
 OC Viruses; ssRNA negative-strand viruses; Mononegavirales;
 OC Paramyxoviridae; Paramyxovirinae; Rubulavirus.
 OX NCBI_TaxID=11190;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=89171450; PubMed=3351479;
 RA Millar N.S., Chambers P., Emerson P.T.;
 RT "Nucleotide sequence of the fusion and haemagglutinin-neuraminidase
 RT glycoprotein genes of Newcastle disease virus, strain Ulster;
 RT molecular basis for variations in pathogenicity between strains.";
 RL J. Gen. Virol. 69:613-620(1988).
 RN [2]

RP SEQUENCE FROM N.A.
 RX MEDLINE=89204898; PubMed=2705298;
 RA Toyoda T., Sakaguchi T., Hirota H., Gotoh B., Kuma K., Miyata T.,
 RA Nagai Y.;
 RT "Newcastle disease virus evolution. II. Lack of gene recombination in
 RT generating virulent and avirulent strains.";
 RL Virology 169:273-282(1989).
 CC -1- FUNCTION: This protein directs fusion of viral and cellular
 CC membranes.
 CC -1- SUBUNIT: THE MATURE FORM IS A DIMER OF POLYPEPTIDES F-1 AND F-2
 CC LINKED BY A DISULFIDE BOND.
 CC -1- SIMILARITY: Belongs to the paramyxoviruses fusion glycoprotein
 CC family.
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 CC -----
 DR EMBL; D00243; BAA00173.1; -;
 DR EMBL; M24694; AAA46645.1; -;
 DR PIR; A29823; VGNZU1.
 DR InterPro: IPR00076; Fusion gly.
 DR Pfam; PF00523; Fusion_gly, 1.
 DR Glycoprotein; Fusion protein; Transmembrane; Envelope protein; Signal;
 KW Lipoprotein; Palmitate.
 FT SIGNAL 1 25
 FT CHAIN 26 553 FUSION GLYCOPROTEIN F0.
 FT CHAIN 26 116 F2 PROTEIN.
 FT CHAIN 117 553 F1 PROTEIN.
 FT TRANSMEM 117 136 POTENTIAL.
 FT DOMAIN 137 500 EXTRACELLULAR.
 FT TRANSMEM 501 527 POTENTIAL.
 FT DOMAIN 528 553 CYTOPLASMIC.
 FT CARBOHYD 85 85 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 191 191 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 366 366 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 447 471 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 471 471 S-palmitoyl cysteine (in host)
 FT LIPID 523 523 (Potential).
 SQ SEQUENCE 553 AA; 58682 MW; FC99C763D8E2F7FA CRC64;
 Query Match 98.8%; Score 2724; DB 1; Length 553;
 Best Local Similarity 99.1%; Pred. No. 2.5e-162;
 Matches 548; Conservative 1; Mismatches 4; Indels 0; Gaps 0;
 QY 1 MGRSSSTRIPVPLMLTVRVALALSCVPTSSLDGRPLAAAGIVVTGKAVNIYTSQTGS 60
 DB 1 MGRSSSTRIPVPLMLTVRVALALSCVPTSSLDGRPLAAAGIVVTGKAVNIYTSQTGS 60
 QY 61 IIVKLLNMPKDEKACAKAPLEAYNRTLTLLTFLGDSIRRIQSVTSSGGKQRLIGA 120
 DB 61 IIVKLLNMPKDEKACAKAPLEAYNRTLTLLTFLGDSIRRIQSVTSSGGKQRLIGA 120
 QY 121 IIGGAALGVATAAQTAAALIQANQNAANILRLKERIAATNEAVHEVTDGLSOLAVAVG 180
 DB 121 IIGGAALGVATAAQTAAALIQANQNAANILRLKERIAATNEAVHEVTDGLSOLAVAVG 180
 QY 181 KMQQFVNDQFNKTAQELDCIKITQOVGVNELMLYLTELTTVFGPQITSPALTIQALYN 240
 DB 181 KMQQFVNDQFNKTAQELDCIKITQOVGVNELMLYLTELTTVFGPQITSPALTIQALYN 240
 QY 241 LAGNMDYLLTKLGVGNQLSSGLITGNPILYDSQTOLLGIQVTLPSVGNLNNMRA 300
 DB 241 LAGNMDYLLTKLGVGNQLSSGLITGNPILYDSQTOLLGIQVTLPSVGNLNNMRA 300
 QY 301 TYLETSLVSTTKGFASALVPKVMKGVSVIEELDTSYCIETDLDLYCTRIVTFPMSPGIY 360
 DB 301 TYLETSLVSTTKGFASALVPKVMKGVSVIEELDTSYCIETDLDLYCTRIVTFPMSPGIY 360


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QY 361 SCLSGNTSACMSYKTEGALTPYMTLKGSVIANCKMTTCRCADPPGIISQNYGEAVSLID 420
Db 361 SCLSGNTSACMSYKTEGALTPYMTLKGSVIANCKMTTCRCADPPGIISQNYGEAVSLID 420
QY 421 RQCNVLSLDGITLRLSGEPDATYQKNISIQDSQVIVTGNLDISTELGNVNSISNALDK 480
Db 421 RQCNVLSLDGITLRLSGEPDATYQKNISIQDSQVIVTGNLDISTELGNVNSISNALDK 480
QY 481 LEESNSKLDKVNKLTSTSLITYVILTVISLVCGLISLVACLYMYKQKAQKQKTLMLWG 540
Db 481 LEESNSKLDKVNKLTSTSLITYVILTVISLVCGLISLVACLYMYKQKAQKQKTLMLWG 540
QY 541 NNTLDQMRATTKM 553
Db 541 NNTLDQMRATTKM 553

RESULT 3
VGLF NDVQ
ID VGLF NDVQ STANDARD; PRT; 553 AA.
AC P33615;
DT 01-FEB-1994 (Rel. 28, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Fusion glycoprotein precursor [Contains: Fusion glycoprotein F2;
DE Fusion glycoprotein F1].
GN F.
OS Newcastle disease virus (strain Queensland/66) (NDV).
OC Viruses; ssRNA negative-strand viruses; Mononegavirales;
OC Paramyxoviridae; Paramyxovirinae; Rubulavirus.
OX NCBI_TaxID=11186;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=89204898; PubMed=2705298;
RA Toyoda T., Sakaguchi T., Hirota H., Gotoh B., Kuma K., Miyata T.,
RA Nagai Y.;
RT "Newcastle disease virus evolution. II. Lack of gene recombination in
RT generating virulent and avirulent strains.";
RL Virology 169:273-282(1989).
CC -!- FUNCTION: This protein directs fusion of viral and cellular
CC membranes.
CC -!- SUBUNIT: THE MATURE FORM IS A DIMER OF POLYPEPTIDES F-1 AND F-2
CC LINKED BY A DISULFIDE BOND.
CC -!- SIMILARITY: Belongs to the paramyxoviruses fusion glycoprotein
CC family.
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DR EMBL; M24693; AAA46644.1; --
DR PIR; B46329; B46329.
DR InterPro; IPR000776; Fusion_gly.
DR Pfam; PF00523; fusion_gly; 1.
KW Glycoprotein; Fusion protein; Transmembrane; Envelope protein; Signal;
KW Lipoprotein; Palmitate.
SIGNAL 1 25
FT CHAIN 26 553 FUSION GLYCOPROTEIN F0.
FT CHAIN 26 116 F2 PROTEIN.
FT CHAIN 117 553 F1 PROTEIN.
FT TRANSMEM 117 136 POTENTIAL.
FT DOMAIN 137 500 EXTRACELLULAR.
FT TRANSMEM 501 527 POTENTIAL.
FT DOMAIN 528 553 CYTOPLASMIC.
FT CARBOHYD 85 85 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 191 191 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 366 366 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 447 447 N-LINKED (GLCNAC. . .) (POTENTIAL).

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FT CARBOHYD 471 471 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT LIPID 523 523 S-palmitoyl cysteine (in host)
FT FT (Potential).
SQ SEQUENCE 553 AA; 58866 MW; 38144816A45B3EF7 CRC64;

Query Match 97.4%; Score 2684; DB 1; Length 553;
Best Local Similarity 97.3%; Pred. No. 7.7e-160;
Matches 538; Conservative 7; Mismatches 8; Indels 0; Gaps 0;

QY 1 MGRSSRTRIPVPLMLTVRVALALSCVPTSSLDGRPLAAAGIVVTGKAVNIYTSSTGTS 60
Db 1 MGRSSRTRIPVPLMLTVRVALALSCVPTSSLDGRPLAAAGIVVTGKAVNIYTSSTGTS 60
QY 61 IIVKLLNMPKDKKACAKAPLEAYNRTLTLLTPGDSIRRIQESVTTSGGKQGRLLGA 120
Db 61 IIVKLLNMPKDKKACAKAPLEAYNRTLTLLTPGDSIRRIQESVTTSGGKQGRLLGA 120
QY 121 IIGGAALGVATAAQITAAASALIOANQNAANLRLKERIAATNEAVHEVTGSLQAVAG 180
Db 121 IIGGAALGVATAAQITAAASALIOANQNAANLRLKERIAATNEAVHEVTGSLQAVAG 180
QY 181 KMQQFVNDQFNKTAQELDCIKITQQVGVNELNLYLTETTTVFGPQITSPALTIQALYN 240
Db 181 KMQQFVNDQFNKTAQELDCIKITQQVGVNELNLYLTETTTVFGPQITSPALTIQALYN 240
QY 241 LAGNMDYLLTKLGVGNQNLSSLISSGLITGNPILYDSQTLGLGIQVTLPSVGNLNNRA 300
Db 241 LAGNMDYLLTKLGVGNQNLSSLISSGLITGNPILYDSQTLGLGIQVTLPSVGNLNNRA 300
QY 301 TYLETLSVSTTKGFASALVPKVMKGVSVIEELDTSCYIETDLDLYCTRTVTPMSPGIY 360
Db 301 TYLETLSVSTTKGFASALVPKVMKGVSVIEELDTSCYIETDLDLYCTRTVTPMSPGIY 360
QY 361 SCLSGNTSACMSYKTEGALTPYMTLKGSVIANCKMTTCRCADPPGIISQNYGEAVSLID 420
Db 361 SCLSGNTSACMSYKTEGALTPYMTLKGSVIANCKMTTCRCADPPGIISQNYGEAVSLID 420
QY 421 RQCNVLSLDGITLRLSGEPDATYQKNISIQDSQVIVTGNLDISTELGNVNSISNALDK 480
Db 421 RQCNVLSLDGITLRLSGEPDATYQKNISIQDSQVIVTGNLDISTELGNVNSISNALDK 480
QY 481 LEESNSKLDKVNKLTSTSLITYVILTVISLVCGLISLVACLYMYKQKAQKQKTLMLWG 540
Db 481 LEESNSKLDKVNKLTSTSLITYVILTVISLVCGLISLVACLYMYKQKAQKQKTLMLWG 540
QY 541 NNTLDQMRATTKM 553
Db 541 NNTLDQMRATTKM 553

RESULT 4
VGLF NDVH4
ID VGLF NDVH4 STANDARD; PRT; 553 AA.
AC P33613;
DT 01-FEB-1994 (Rel. 28, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Fusion glycoprotein precursor [Contains: Fusion glycoprotein F2;
DE Fusion glycoprotein F1].
GN F.
OS Newcastle disease virus (strain B1-Hitchner/47) (NDV).
OC Viruses; ssRNA negative-strand viruses; Mononegavirales;
OC Paramyxoviridae; Paramyxovirinae; Rubulavirus.
OX NCBI_TaxID=11181;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=89204898; PubMed=2705298;
RA Toyoda T., Sakaguchi T., Hirota H., Gotoh B., Kuma K., Miyata T.,
RA Nagai Y.;
RT "Newcastle disease virus evolution. II. Lack of gene recombination in
RT generating virulent and avirulent strains.";
RL Virology 169:273-282(1989).
CC -!- FUNCTION: This protein directs fusion of viral and cellular

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FT CARBOHYD 471 471 N-LINKED (GLCNAC. . .) (POTENTIAL) .
FT LIPID 523 523 S-palmitoyl cysteine (in host)
FT FT (Potential) .
FT CONFLICT 66 66 H -> L (IN REF. 2) .
FT CONFLICT 162 162 I -> N (IN REF. 2) .
SQ SEQUENCE 553 AA; 59022 MW; 0777BF9B6B1D1D27 CRC64;

Query Match 95.0%; Score 2618; DB 1; Length 553;
Best Local Similarity 95.3%; Pred. No. 9.9e-156;
Matches 52; Conservative 6; Mismatches 20; Indels 0; Gaps 0;

QY 1 MGRSSTRIPVPLMLTVRVVALALSCVCPSTSLDGRPLAAAGIVVTGDKAVNIYTSSTQGS 60
DB 1 MGPSSSTRIPVPLMLTVRIALALSCVHSLDGRPLAAAGIVVTGDKAVNIYTSSTQGS 60
QY 61 IIVKLLPNMPKDKACAKAPLEAYNRLTLLTLLPLGDSIRRIQSVVTSSTGGKQRLIGA 120
DB 61 IIVKLLPNMPKDKACAKAPLEAYNRLTLLTLLPLGDSIRRIQSVVTSSTGGKQRLIGA 120
QY 121 IIGGAALGVATAAQITAAASALIQAQNAANILRLKERIAATNEAVHEVTDGLSOLAVAG 180
DB 121 IIGSVALGVATAAQITAAASALIQAQNAANILRLKESIAATNEAVHEVTDGLSOLAVAG 180
QY 181 KMQQFVNDQFNKTAQELDCIKITQOVGVNELNLYLTLLTVPQITSPALTIQALYN 240
DB 181 KMQQFVNDQFNNTAQELDCIKITQOVGVNELNLYLTLLTVPQITSPALTIQALYN 240
QY 241 LAGGNMDYLLTKLGVGNQNLSSLIIGSLITGNPILYDSOTQLLGIQVTLPSVGNLNMRA 300
DB 241 LAGGNMDYLLTKLGVGNQNLSSLIIGSLITGNPILYDSOTQLLGIQVTLPSVGNLNMRA 300
QY 301 TYLETLSVSTTKGFASALVPKVMKGVSVIEELDTSYCIETDLDLYCTRIVTFPMSPGIY 360
DB 301 TYLETLSVSTTKGFASALVPKVMKGVSVIEELDTSYCIETDLDLYCTRIVTFPMSPGIY 360
QY 361 SCLSGNTSACWYKTEGALTTPYMTLKGSVIANCKMTTCRCADPPGIISQNYGEAVSLID 420
DB 361 SCLNGNTSACWYKTEGALTTPYMTLKGSVIANCKMTTCRCADPPGIISQNYGEAVSLID 420
QY 421 RQSCNVLSLGGITLRLSGFDATYQKNISIQDSQVIVTGNLIDSTELGNVNSISNALDK 480
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QY 481 LBSNSKLDKVNKLTSTSLITVITVLSVCGILSLVLACVLMYKOKAQOKTLWLIG 540
DB 481 LBSNSKLDKVNKLTSTSLITVITVLSVCGILSLVLACVLMYKOKAQOKTLWLIG 540
QY 541 NNTLDQMRATTXM 553
DB 541 NNTLGQMRATTXM 553

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RESULT 6
VGLF_NDVT STANDARD; PRT; 553 AA.
ID VGLF_NDVT
AC P26628;
DT 01-AUG-1992 (Rel. 23, Created)
DT 01-AUG-1992 (Rel. 23, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Fusion glycoprotein precursor [Contains: Fusion glycoprotein F2;
DE Fusion glycoprotein F1].
GN F.
OS Newcastle disease virus (strain Texas) (NDV).
OC Viruses; ssRNA negative-strand viruses; Mononegavirales;
OC Paramyxoviridae; Paramyxovirinae; Rubulavirus.
OX NCBI_TaxID=11188;
RN [1]
RP SEQUENCE FROM N. A.
RX MEDLINE=90204652; PubMed=2157037;
RA Taylor J., Edbauer C., Rey-Senelange A., Bouquet J.F., Norton E.,
RA Goebel S., Desmettre P., Paolletti E.;
RT "Newcastle disease virus fusion protein expressed in a fowlpox virus
recombinant confers protection in chickens.";

```

```

J. Virol. 64:1441-1450 (1990).
-!- FUNCTION: This protein directs fusion of viral and cellular
membranes.
-!- SUBUNIT: THE MATURE FORM IS A DIMER OF POLYPEPTIDES F-1 AND F-2
LINKED BY A DISULFIDE BOND.
-!- SIMILARITY: Belongs to the paramyxoviruses fusion glycoprotein
family.

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EMBL; M33855; AAA46675.1; -.
PIR; A34663; VGNZTE.
InterPro; IPR000776; Fusion_gly.
Pfam; PF00523; Fusion_gly; 1.
KW Glycoprotein; Fusion protein; Transmembrane; Envelope protein; Signal;
Lipoprotein; Palmitate.
FT SIGNAL 1 25
FT CHAIN 26 553 FUSION GLYCOPROTEIN F0.
FT CHAIN 26 116 F2 PROTEIN.
FT CHAIN 117 553 F1 PROTEIN.
FT TRANSMEM 117 136 POTENTIAL.
FT DOMAIN 137 500 EXTRACELLULAR.
FT TRANSMEM 501 527 POTENTIAL.
FT DOMAIN 528 553 CYTOPLASMIC.
FT CARBOHYD 85 85 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 191 191 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 366 366 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 447 447 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 471 471 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT LIPID 523 523 S-palmitoyl cysteine (in host)
SQ SEQUENCE 553 AA; 59042 MW; 4D335F8E159757B7 CRC64;

Query Match 94.5%; Score 2606; DB 1; Length 553;
Best Local Similarity 94.8%; Pred. No. 5.6e-155;
Matches 524; Conservative 9; Mismatches 20; Indels 0; Gaps 0;

QY 1 MGRSSTRIPVPLMLTVRVVALALSCVCPSTSLDGRPLAAAGIVVTGDKAVNIYTSSTQGS 60
DB 1 MGRSSTRIPVPLMLTIRALTALTSCLRTSSLDGRPLAAAGIVVTGDKAVNIYTSSTQGS 60
QY 61 IIVKLLPNMPKDKACAKAPLEAYNRLTLLTLLPLGDSIRRIQSVVTSSTGGKQRLIGA 120
DB 61 IIVKLLPNMPKDKACAKAPLEAYNRLTLLTLLPLGDSIRRIQSVVTSSTGGKQRLIGA 120
QY 121 IIGGAALGVATAAQITAAASALIQAQNAANILRLKERIAATNEAVHEVTDGLSOLAVAG 180
DB 121 IIGSVALGVATAAQITAAASALIQAQNAANILRLKESIAATNEAVHEVTDGLSOLAVAG 180
QY 181 KMQQFVNDQFNKTAQELDCIKITQOVGVNELNLYLTLLTVPQITSPALTIQALYN 240
DB 181 KMQQFVNDQFNNTAQELDCIKITQOVGVNELNLYLTLLTVPQITSPALTIQALYN 240
QY 241 LAGGNMDYLLTKLGVGNQNLSSLIIGSLITGNPILYDSOTQLLGIQVTLPSVGNLNMRA 300
DB 241 LAGGNMDYLLTKLGVGNQNLSSLIIGSLITGNPILYDSOTQLLGIQVTLPSVGNLNMRA 300
QY 301 TYLETLSVSTTKGFASALVPKVMKGVSVIEELDTSYCIETDLDLYCTRIVTFPMSPGIY 360
DB 301 TYLETLSVSTTKGFASALVPKVMKGVSVIEELDTSYCIETDLDLYCTRIVTFPMSPGIY 360
QY 361 SCLSGNTSACWYKTEGALTTPYMTLKGSVIANCKMTTCRCADPPGIISQNYGEAVSLID 420
DB 361 SCLSGNTSACWYKTEGALTTPYMTLKGSVIANCKMTTCRCADPPGIISQNYGEAVSLID 420
QY 421 RQSCNVLSLGGITLRLSGFDATYQKNISIQDSQVIVTGNLIDSTELGNVNSISNALDK 480

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Db 421 RHSCNVLSLDGTTIRLSGEFDATYQKNISILDSQVIVTGNLDISTELGNVNNISNALNK 480
 Qy 481 LEENSXKLDKVNKLTSTTSALITYIVLTIVSLVCGILSLVACLYMYKQKQKQKTLMLG 540
 Db 481 LEENSXKLDKVNKLTSTTSALITYIVLTIVSLVCGILSLVACLYMYKQKQKQKTLMLG 540
 Qy 541 NNTLDQMRATTM 553
 Db 541 NNTLDQMRATTM 553

RESULT 7
 VGLF NDVB
 ID VGLF NDVB STANDARD; PRT; 553 AA.
 AC P06156;
 DT 01-JAN-1988 (Rel. 06, Created)
 DT 01-JAN-1988 (Rel. 06, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Fusion glycoprotein precursor [Contains: Fusion glycoprotein F2;
 DE Fusion glycoprotein F1].
 GN F.
 OS Newcastle disease virus (strain Beaudette C/45) (NDV).
 OC Viruses; ssRNA negative-strand viruses; Mononegavirales;
 OC Paramyxoviridae; Paramyxovirinae; Rubulavirus.
 OX NCBI_TaxID=11178;
 RN [1]
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=87085486; PubMed=3025345;
 RA Chambers P., Millar N.S., Emmerson P.T.;
 RA "Nucleotide sequence of the gene encoding the fusion glycoprotein of
 RT Newcastle disease virus.";
 RL J. Gen. Virol. 67:2685-2694 (1986).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=89204898; PubMed=2705298;
 RA Toyoda T., Sakaguchi T., Hirota H., Gotoh B., Kuma K., Miyata T.,
 RA Nagai Y.;
 RA "Newcastle disease virus evolution. II. Lack of gene recombination in
 RT generating virulent and avirulent strains.";
 RL Virology 169:273-282 (1989).
 CC -!- FUNCTION: This protein directs fusion of viral and cellular
 CC membranes.
 CC -!- SUBUNIT: THE MATURE FORM IS A DIMER OF POLYPEPTIDES F-1 AND F-2
 CC LINKED BY A DISULFIDE BOND.
 CC -!- SIMILARITY: Belongs to the paramyxoviruses fusion glycoprotein
 CC family.

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 DB EMBL; X04719; CAA28426.1; -
 DB EMBL; M24697; ARA46648.1; -
 DB EMBL; A03663; CAA00288.1; -
 DB F1R; A27008; VGNZNV.
 DE InterPro; IPR000776; Fusion gly.
 DE Pfam; PF00523; fusion gly; 1.
 DE Lipoprotein; Fusion protein; Transmembrane; Envelope protein; Signal;
 DE Lipoprotein; Palmitate.
 FT SIGNAL
 FT CHAIN 1 25
 FT CHAIN 26 553
 FT CHAIN 26 116
 FT CHAIN 117 553
 FT CHAIN 117 136
 FT DOMAIN 137 500
 FT DOMAIN 501 527
 FT DOMAIN 528 553
 FT CARBOHYD 85 85
 FT CARBOHYD 191 191

FT CARBOHYD 366 366 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 447 447 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 471 471 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT LIPID 523 523 S-palmitoyl cysteine (in host)
 FT (Potential).
 SQ SEQUENCE 553 AA; 59041 MW; 63BFD1692AFDE191 CRC64;
 Query Match 94.4%; Score 2603; DB 1; Length 553;
 Best Local Similarity 93.5%; Pred. No. 8.5e-155;
 Matches 517; Conservative 19; Mismatches 17; Indels 0; Gaps 0;
 Qy 1 MGRSSSTRIPVPLMLTVRVALALSCVCPSTSSLDGRPLAAAGIVVTGKAVNIYSSQTS 60
 Db 1 MGRPSTYKXNPVPMMLTVRVALVLSICIPANSIDGRPLAAAGIVVTGKAVNIYSSQTS 60
 Qy 61 IIVKLLNMPKDKKACAKAPLEAYNRTLTLLTPLGDSIRIRIQESVTTSGGKGRLIGA 120
 Db 61 IIVKLLNPNLPKDKKACAKAPLDAYNRTLTLLTPLGDSIRIRIQESVTTSGGKRKFIGA 120
 Qy 121 IIGGALGVATAAQITTAASALIQAQNAANTLRKERTAAATNEAVHEVTDGLSOLAVAG 180
 Db 121 IIGGVALGVATAAQITTAALIIQAQNAANTLRKESAAATNEAVHEVTDGLSOLAVAG 180
 Qy 181 KMQOFVNDQFNKTAQELDCIKITQOVGVLEMLYLTETTFVFPQITSPALTQTITQALYN 240
 Db 181 KMQOFVNDQFNKTAQELGCIIRIAQOVGVLEMLYLTETTFVFPQITSPALNKLTITQALYN 240
 Qy 241 LAGNMVYLLPKLGVNNQLSSLTGSLITGNPILYDSOTQLGLQVTLPSVGNLNNMRA 300
 Db 241 LAGNMVYLLPKLGVNNQLSSLTGSLITGNPILYDSOTQLGLQVTLPSVGNLNNMRA 300
 Qy 301 TYLETSLVSTTKGFASALVPKVMKGVSVIEELTDSYCIETDLDLYCYTRIVTFPMSPGIY 360
 Db 301 TYLETSLVSTTRGFASALVPKVTQVGSVIEELTDSYCIETDLDLYCYTRIVTFPMSPGIY 360
 Qy 361 SCLSGNTSACMYSKTEGALTTPYMTLKGSVIANCMTTCRCADPPGIISQNYGEAVSLID 420
 Db 361 SCLSGNTSACMYSKTEGALTTPYMTIKGSVIANCMTTCRCVNPFGIISQNYGEAVSLID 420
 Qy 421 RQSCNVLSLDGTTIRLSGEFDATYQKNISILDSQVIVTGNLDISTELGNVNNISNALDK 480
 Db 421 RQSCNVLSLDGTTIRLSGEFDATYQKNISILDSQVIVTGNLDISTELGNVNNISNALNK 480
 Qy 481 LEENSXKLDKVNKLTSTTSALITYIVLTIVSLVCGILSLVACLYMYKQKQKQKTLMLG 540
 Db 481 LEENSXKLDKVNKLTSTTSALITYIVLTIVSLVCGILSLVACLYMYKQKQKQKTLMLG 540
 Qy 541 NNTLDQMRATTM 553
 Db 541 NNTLDQMRATTM 553

RESULT 8

VGLF NDVB
 ID VGLF NDVB3 STANDARD; PRT; 553 AA.
 AC P33612;
 DT 01-PEB-1994 (Rel. 28, Created)
 DT 01-PEB-1994 (Rel. 28, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Fusion glycoprotein precursor [Contains: Fusion glycoprotein F2;
 DE Fusion glycoprotein F1].
 GN F.
 OS Newcastle disease virus (strain Her/33) (NDV).
 OC Viruses; ssRNA negative-strand viruses; Mononegavirales;
 OC Paramyxoviridae; Paramyxovirinae; Rubulavirus.
 OX NCBI_TaxID=11187;
 RN [1]
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=89204898; PubMed=2705298;
 RA Toyoda T., Sakaguchi T., Hirota H., Gotoh B., Kuma K., Miyata T.,
 RA Nagai Y.;
 RA "Newcastle disease virus evolution. II. Lack of gene recombination in
 RT generating virulent and avirulent strains.";
 RL Virology 169:273-282 (1989).
 CC -!- FUNCTION: This protein directs fusion of viral and cellular
 CC membranes.
 CC -!- SUBUNIT: THE MATURE FORM IS A DIMER OF POLYPEPTIDES F-1 AND F-2
 CC LINKED BY A DISULFIDE BOND.
 CC -!- SIMILARITY: Belongs to the paramyxoviruses fusion glycoprotein
 CC family.

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 DB EMBL; X04719; CAA28426.1; -
 DB EMBL; M24697; ARA46648.1; -
 DB EMBL; A03663; CAA00288.1; -
 DB F1R; A27008; VGNZNV.
 DE InterPro; IPR000776; Fusion gly.
 DE Pfam; PF00523; fusion gly; 1.
 DE Lipoprotein; Fusion protein; Transmembrane; Envelope protein; Signal;
 DE Lipoprotein; Palmitate.
 FT SIGNAL
 FT CHAIN 1 25
 FT CHAIN 26 553
 FT CHAIN 26 116
 FT CHAIN 117 553
 FT CHAIN 117 136
 FT DOMAIN 137 500
 FT DOMAIN 501 527
 FT DOMAIN 528 553
 FT CARBOHYD 85 85
 FT CARBOHYD 191 191


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PT CARBOHYD 366 366 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 447 447 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 471 471 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT LIPID 523 523 S-palmitoyl cysteine (in host)
                                         (potential).
SQ SEQUENCE 553 AA; 59017 MW; 5F537269FE76F9E9 CRC64;

Query Match 94.1%; Score 2593; DB 1; Length 553;
Best Local Similarity 93.1%; Pred. No. 3.6e-154;
Matches 515; Conservative 19; Mismatches 19; Indels 0; Gaps 0;

QY 1 MGRSRSTRIPVPLMLTVRVALALSCVPTSSLDGRPLAAAGIVVTGDKAVNIYTSQTGS 60
DB 1 MGPRSTKNTPTPMLTVRVALVLSICFANIDGRPLAAAGIVVTGDKAVNIYTSQTGS 60

QY 61 IIVKLLPNMPKDEKACAPLEAYNRTLTLLTPLGDSIRRIQESVTTSGGKGQRLIGA 120
DB 61 IIVKLLPNMPKDEKACAPLEAYNRTLTLLTPLGDSIRRIQESVTTSGGKGQRLIGA 120

QY 121 IIGGAALGVATAAQITTAASALIQANNAANILRLKERTAAATNEAHEVTDGLSOLAVAG 180
DB 121 IIGGAALGVATAAQITTAASALIQANNAANILRLKERTAAATNEAHEVTDGLSOLAVAG 180

QY 121 IIGGVALGVATAAQITTAASALIQANNAANILRLKESIAATNEAHEVTDGLSOLAVAG 180
DB 121 IIGGVALGVATAAQITTAASALIQANNAANILRLKESIAATNEAHEVTDGLSOLAVAG 180

QY 181 KMQQFVNDQFNKTAQELDCIKITQOVGVNELNLYLTTELTVFGPQITSPALTOITQALYN 240
DB 181 KMQQFVNDQFNKTAQELDCIKITQOVGVNELNLYLTTELTVFGPQITSPALTOITQALYN 240

QY 241 LAGGNDYLLTKLGVGNQLSGLITGNPILYDSOTQLLGIQVTLPSVGNLNNMRA 300
DB 241 LAGGNDYLLTKLGVGNQLSGLITGNPILYDSOTQLLGIQVTLPSVGNLNNMRA 300

QY 301 TYLETSLVSTTKGFASALVPKVMKGVSVIEELDTSYCIETDLDLYCYTRIVTFPMSPGIY 360
DB 301 TYLETSLVSTTKGFASALVPKVMKGVSVIEELDTSYCIETDLDLYCYTRIVTFPMSPGIY 360

QY 361 SCLSGNTSACMSYKTEGALTTPYMTLKGSVIANCKMTTCRCADPPGIISQNYGEAVSLID 420
DB 361 SCLSGNTSACMSYKTEGALTTPYMTLKGSVIANCKMTTCRCVNPFGISQNYGEAVSLID 420

QY 421 ROSCNVLSIDGTLRLSGFDATYQKNISIQDSQVIVTGNLIDISTELGNVNNISNALDK 480
DB 421 KQSCNVLSIDGTLRLSGFDATYQKNISIQDSQVIVTGNLIDISTELGNVNNISNALNK 480

QY 481 LEESKLDKNNVLTSTTSALITYLVTLVSVLCGLISLVACLYMYKKAQOKTLMLG 540
DB 481 LEESKLDKNNVLTSTTSALITYLVTLVSVLCGLISLVACLYMYKKAQOKTLMLG 540

QY 541 NNTLDQMRATTKM 553
DB 541 NNTLDQMRATTKM 553
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RESULT 10
VGLF NDVI STANDARD; PRT; 553 AA.
AC P14623;
DT 01-APR-1990 (Rel. 14, Created)
DT 01-APR-1990 (Rel. 14, Last sequence update)
DE Fusion glycoprotein precursor [Contains: Fusion glycoprotein F2;
DE Fusion glycoprotein F1].
GN F.
OS Newcastle disease virus (strain Italien/45) (NDV).
OC Viruses; ssRNA negative-strand viruses; Mononegavirales;
OC Paramyxoviridae; Paramyxovirinae; Rubulavirus.
OX NCBI_TaxID=11182;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=87240797; PubMed=3592986;
RA Espion D., de Henau S., Letellier C., Wemmers C.-D., Brasseur R.,
RA Young J.F., Gross M., Rosenberg M., Meulemans G., Burny A.;
RT "Expression at the cell surface of native fusion protein of the
RT Newcastle disease virus (NDV) strain Italien from cloned cDNA.";
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```
Arch. Virol. 95:79-95 (1987).
[2]
SEQUENCE FROM N.A.
MEDLINE=89204898; PubMed=2705298;
RA Toyoda T., Sakaguchi T., Hirota H., Gotoh B., Kuma K., Miyata T.,
RA Nagai Y.;
RT "Newcastle disease virus evolution. II. Lack of gene recombination in
RT generating virulent and avirulent strains.";
RL Virology 169:273-282 (1989). directs fusion of viral and cellular
CC -!- FUNCTION: This protein directs fusion of viral and cellular
CC membranes.
CC -!- SUBUNIT: THE MATURE FORM IS A DIMER OF POLYPEPTIDES F-1 AND F-2
CC LINKED BY A DISULFIDE BOND.
CC -!- SIMILARITY: Belongs to the paramyxoviruses fusion glycoprotein
CC family.
CC
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL; M17710; AAA46640.1; -.
DR EMBL; M24703; AAA46653.1; ALT_SEQ.
DR PIR; B36830; B36830.
DR InterPro; IPR000776; Fusion_gly.
DR Pfam; PF00523; fusion_gly; 1.
KW Glycoprotein; Fusion protein; Transmembrane; Envelope protein; Signal;
KW Lipoprotein; Palmitate.
FT SIGNAL 1 25
FT CHAIN 26 553 FUSION GLYCOPROTEIN FO.
FT CHAIN 26 116 F2 PROTEIN.
FT CHAIN 117 553 F1 PROTEIN.
FT TRANSMEM 117 136 POTENTIAL.
FT DOMAIN 137 500 EXTRACELLULAR.
FT TRANSMEM 501 527 POTENTIAL.
FT DOMAIN 528 553 CYTOPLASMIC.
FT CARBOHYD 85 85 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 191 191 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 366 366 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 447 447 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 471 471 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT LIPID 523 523 S-palmitoyl cysteine (in host)
                                         (Potential).
FT CONFLICT 289 290 SP -> LS (IN REF. 2).
FT CONFLICT 339 339 M -> I (IN REF. 2).
FT CONFLICT 491 491 L -> V (IN REF. 2).
SQ SEQUENCE 553 AA; 59260 MW; 639B2F2AE19153E2 CRC64;

Query Match 93.9%; Score 2588; DB 1; Length 553;
Best Local Similarity 93.9%; Pred. No. 7.3e-154;
Matches 519; Conservative 14; Mismatches 20; Indels 0; Gaps 0;

QY 1 MGRSRSTRIPVPLMLTVRVALALSCVPTSSLDGRPLAAAGIVVTGDKAVNIYTSQTGS 60
DB 1 MGRSRSTRIPVPLMLTVRVALALSCVPTSSLDGRPLAAAGIVVTGDKAVNIYTSQTGS 60

QY 61 IIVKLLPNMPKDEKACAPLEAYNRTLTLLTPLGDSIRRIQESVTTSGGKGQRLIGA 120
DB 61 IIVKLLPNMPKDEKACAPLEAYNRTLTLLTPLGDSIRRIQESVTTSGGKGQRLIGA 120

QY 121 IIGGAALGVATAAQITTAASALIQANNAANILRLKERTAAATNEAHEVTDGLSOLAVAG 180
DB 121 IIGGVALGVATAAQITTAASALIQANNAANILRLKESIAATNEAHEVTDGLSOLAVAG 180

QY 181 KMQQFVNDQFNKTAQELDCIKITQOVGVNELNLYLTTELTVFGPQITSPALTOITQALYN 240
DB 181 KMQQFVNDQFNKTAQELDCIKITQOVGVNELNLYLTTELTVFGPQITSPALTOITQALYN 240

QY 241 LAGGNDYLLTKLGVGNQLSGLITGNPILYDSOTQLLGIQVTLPSVGNLNNMRA 300
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Db 241 LAGNMDYLLTKLGVGNQSLISGLITGNPIYDSQTLGIQITSPSVGNLNNMRA 300
Qy 301 TYLETLSVSTTKGFASALVPKVMKGVSVIEELDTSYCIETDLDLYCTRIIVTFPMSPGIY 360
Db 301 TYLETLSVSTTKGFASALVPKVMKGVSVIEELDTSYCMETDLDLYCTRIIVTFPMSPGIY 360
Qy 361 SCLSNVSACMYSKTEGALTPYMTLKGSVIANCWMTTCRCADPGIISQNYGEAVSLID 420
Db 361 SCLSGNTSACMYSKTEGALTPYMTLKGSVIANCWMTTCRCADPGIISQNYGEAVSLID 420
Qy 421 RQSCNVLSLDGITLRLSGFEFDATYQKNISIQDSOVIVTGNLIDISTELGNVNSISNALDK 480
Db 421 RHSCNVLSLDGITLRLSGFEFDATYQKNISILDSQVIVTGNLIDISTELGNVNSISNALNK 480
Qy 481 LEESNSKLDKVNKLTSTSAITIVLVISLVCGILSLVLAACYLMYKQKQAQKTLMLWG 540
Db 481 LEESNSKLDKVNKLTSTSAITIVLVISLVFGVLSVLVLAACYLMYKQKQAQKTLMLWG 540
Qy 541 NNTLDQMRATTKM 553
Db 541 NNTLDQMRATTKI 553

RESULT 11
VGLF NDVL
ID VGLF NDVL STANDARD; PRT; 553 AA.
AC P33614;
DT 01-FEB-1994 (Rel. 28, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Fusion glycoprotein precursor [Contains: Fusion glycoprotein F2;
DE Fusion glycoprotein F1].
GN F.
OS Newcastle disease virus (strain Las/46) (NDV).
OC Viruses; ssRNA negative-strand viruses; Mononegavirales;
OC Paramyxoviridae; Paramyxovirinae; Rubulavirus.
OX NCBI_TaxID=11184;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=89204898; PubMed=2705298;
RA Toyoda T., Sakaguchi T., Hirota H., Gotoh B., Kuma K., Miyata T.,
RA Nagai Y.;
RT "Newcastle disease virus evolution. II. Lack of gene recombination in
RT generating virulent and avirulent strains.";
RL Virology 169:273-282(1989).
CC -!- FUNCTION: This protein directs fusion of viral and cellular
CC membranes.
CC -!- SUBUNIT: THE MATURE FORM IS A DIMER OF POLYPEPTIDES F-1 AND F-2
CC LINKED BY A DISULFIDE BOND.
CC -!- SIMILARITY: Belongs to the paramyxoviruses fusion glycoprotein
CC family.
CC
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; M24696; AAA46647.1; -.
CC PIR; E46329; E46329.
CC InterPro; IPR000776; Fusion gly.
CC Pfam; PF00523; fusion_gly; 1.
CC Glycoprotein; Fusion protein; Transmembrane; Envelope protein; Signal;
CC Lipoprotein; Palmitate.
CC SIGNAL 1 25
CC CHAIN 26 553 FUSION GLYCOPROTEIN F0.
CC CHAIN 26 116 F2 PROTEIN.
CC CHAIN 117 553 F1 PROTEIN.
CC TRANSMEM 117 136 POTENTIAL.
CC DOMAIN 137 500 EXTRACELLULAR.
CC TRANSMEM 501 527 POTENTIAL.
CC FT
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FT DOMAIN 528 553 CYTOPLASMIC.
FT CARBOHYD 85 85 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 191 191 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 366 366 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 447 447 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 471 471 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 471 471 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT LIPID 523 523 S-palmitoyl cysteine (in host)
SQ SEQUENCE 553 AA; 59047 MW; 04E11F38573B91DF CRC64;

Query Match 93.9%; Score 2588; DB 1; Length 553;
Best Local Similarity 92.6%; Pred. No. 7.3e-154;
Matches 512; Conservative 21; Mismatches 20; Indels 0; Gaps 0;

Qy 1 MGRSSRTRIPVPLMLTVRVALALSCVCPSTSLDGRPLAAGIVVTGKAVNIYTSSTGTS 60
Db 1 MGRSPSTKIPAPMLTIRVALVLSICPANSIDGRPLAAGIVVTGKAVNIYTSSTGTS 60

Qy 61 IIVKLLNMPKDKKACAKAPLEAVNRTLTLLTLPGLDSIRRIQSVTTSGGKQGRLLGA 120
Db 61 IIVKLLNLPKDKKACAKAPLDAYNRTLTLLTLPGLDSIRRIQSVTTSGGKQGRLLGA 120

Qy 121 IIGGAALGVATAAOITAAASALIQANQNAANLRLKERIAATNEAVHEVTDGLSOLAVAG 180
Db 121 IIGVALGVATPAQITAAALIQAKNAANLRLKESIAATNEAVHEVTDGLSOLAVAG 180

Qy 181 KMQQFVNDQFNKTAQELDCIKITQQGVGVELNLYLTETLTTFVFGPOITSPALTLQIALYN 240
Db 181 KMQQFVNDQFNKTAQELDWIKIAQOVGVELNLYLTETLTTFVFGPOITSPAFNKLTIQIALYN 240

Qy 241 LAGNMDYLLTKLGVGNQSLISGLITGNPIYDSQTLGIQITSPSVGNLNNMRA 300
Db 241 LAGNMDYLLTKLGVGNQSLISGLITGNPIYDSQTLGIQITSPSVGNLNNMRA 300

Qy 301 TYLETLSVSTTKGFASALVPKVMKGVSVIEELDTSYCIETDLDLYCTRIIVTFPMSPGIY 360
Db 301 SYLETLSVSTTRGFASALVPKVMKGVSVIEELDTSYCIETDLDLYCTRIIVTFPMSPGIY 360

Qy 361 SCLSGNTSACMYSKTEGALTPYMTLKGSVIANCWMTTCRCADPGIISQNYGEAVSLID 420
Db 361 SCLSGNTSACMYSKTEAALTTPYMTIKSGVIANCMTTCRCVNPFGIISQNYGEAVSLID 420

Qy 421 RQSCNVLSLDGITLRLSGFEFDATYQKNISIQDSOVIVTGNLIDISTELGNVNSISNALDK 480
Db 421 RQSCNVLSLDGITLRLSGFEFDATYQKNISIQDSOVITGNLIDISTELGNVNSISNALNK 480

Qy 481 LEESNSKLDKVNKLTSTSAITIVLVISLVCGILSLVLAACYLMYKQKQAQKTLMLWG 540
Db 481 LEESNRKLDKVNKLTSTSAITIVLVITISLVFGILSLVLAACYLMYKQKQAQKTLMLWG 540

Qy 541 NNTLDQMRATTKM 553
Db 541 NNTLDQMRATTKM 553
```

RESULT 12

```
VGLF NDVM
ID VGLF NDVM STANDARD; PRT; 553 AA.
AC P10855;
DT 01-JUL-1989 (Rel. 11, Created)
DT 01-JUL-1989 (Rel. 11, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Fusion glycoprotein precursor [Contains: Fusion glycoprotein F2;
DE Fusion glycoprotein F1].
GN F.
OS Newcastle disease virus (strain Miyadera/51) (NDV).
OC Viruses; ssRNA negative-strand viruses; Mononegavirales;
OC Paramyxoviridae; Paramyxovirinae; Rubulavirus.
OX NCBI_TaxID=11185;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=87207668; PubMed=3576973;
RA Toyoda T., Sakaguchi T., Imai K., Inocencio N.M., Gotoh B.,
```

RA Hamaguchi M., Nagai Y.;
RT "Structural comparison of the cleavage-activation site of the fusion
RT glycoprotein between virulent and avirulent strains of Newcastle
RL disease virus.";
RN Virology 158:242-247(1987).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=89204898; PubMed=2705298;
RA Toyoda T., Sakaguchi T., Hirota H., Gotoh B., Kuma K., Miyata T.,
RA Nagai Y.;
RT "Newcastle disease virus evolution. II. Lack of gene recombination in
RT generating virulent and avirulent strains.";
RL Virology 169:273-282(1989).
CC -!- FUNCTION: This protein directs fusion of viral and cellular
CC membranes.
CC -!- SUBUNIT: THE MATURE FORM IS A DIMER OF POLYPEPTIDES F-1 AND F-2
CC LINKED BY A DISULFIDE BOND.
CC -!- SIMILARITY: Belongs to the paramyxoviruses fusion glycoprotein
CC family.
CC
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CC
CC
CC EMBL; M18456; AAA46639.1; -;
CC EMBL; M24701; AAA46651.1; -;
CC PIR; A26185; VGNZND.
CC InterPro; IPR000776; Fusion gly.
CC Pfam; PF00523; fusion gly; 1
CC Glycoprotein; Fusion protein; Transmembrane; Envelope protein; Signal;
CC Lipoprotein; Palmitate.
CC
CC SIGNAL 1 25
CC CHAIN 26 553 FUSION GLYCOPROTEIN F0.
CC CHAIN 26 116 F2 PROTEIN.
CC CHAIN 117 553 F1 PROTEIN.
CC TRANSMEM 117 136 POTENTIAL.
CC DOMAIN 137 500 EXTRACELLULAR.
CC DOMAIN 501 527 POTENTIAL.
CC DOMAIN 528 553 CYTOPLASMIC.
CC CARBOHYD 85 85 N-LINKED (GLCNAC. .) (POTENTIAL).
CC CARBOHYD 191 191 N-LINKED (GLCNAC. .) (POTENTIAL).
CC CARBOHYD 192 192 N-LINKED (GLCNAC. .) (POTENTIAL).
CC CARBOHYD 366 366 N-LINKED (GLCNAC. .) (POTENTIAL).
CC CARBOHYD 447 471 N-LINKED (GLCNAC. .) (POTENTIAL).
CC CARBOHYD 471 471 S-palmitoyl cysteine (in host)
CC LIPID 523 523 (Potential).
CC
CC SEQUENCE 553 AA; 59058 MW; 9AEEB7D60A8FAC2A CRC64;
Query Match 93.5%; Score 2579; DB 1; Length 553;
Best Local Similarity 93.5%; Pred. No. 2.7e-153;
Matches 516; Conservative 14; Mismatches 22; Indels 0; Gaps 0;
1 MGRSSTRIPVPLMTVTRVALALSCVPTSSLDGRLAAGIVVTGDKAVNIYTSQTGS 60
1 MASRSSTRIPAPLMTIITWALGCVRLTSSLDGRLAAGIVVTGDKAVNIYTSQTGS 60
61 IIVKLLPNMPKDKKAKAPLEAYNRTLTTLPLGDSIRRIQESVTTSGGKGQRLLGA 120
61 IIVKLLPNMPKDKKAKAPLEAYNRTLTTLPLGDSIRRIQESVTTSGGRRQRFIGA 120
121 IIGGALGVATAAQITAAALIQANQANANILRLKERTAAATNEAHEVTDGLSOLAVAG 180
121 IIGSVALGVATAAQITAAALIQANQANANILRLKESIAATNEAHEVTDGLSOLAVAG 180
181 KMQQFVNDQFNKTAQELDCIKITQGVGVELNLYLTETLVFGPQITSPALQTITQALYN 240
181 KMQQFVNDQFNNTTQELDCIKITHEVGVELNLYLTETLVFGPQITSPALNQTITQALYN 240

QY 241 LAGNMDYLLTKGLGVGNQLSSLIGSLITGNPILYDSQTQLLGIVTLPSVGNLNNMRA 300
DB 241 LAGNMDYLLTKGLGVGNQLSSLIGSLITGNPILYDSQTQLLGIVTLPSVGNLNNMRA 300
QY 301 TYLETLSVSTTKGFASALVPKVMKVGSVIELDTSYCIETDLDLYCTRIVTFPMSPGIY 360
DB 301 TYLETSSVSTTKGFASALVPKVVTVQVGSVIELDTSYCIETDLDLYCTRIVTFPMSPGIY 360
QY 361 SCLSGNTSACVMSKTEGALTTPYMTLKGSVIANCKMTTCRCADPPGIISQNYGEAVSLID 420
DB 361 SCLTGNTSACVMSKTEGALTTPYMTLKGSVIANCKMTTCRCADPPGIISQNYGEAVSLID 420
QY 421 RQSCNVLSLDGITLRLSGEFDATYQKNISIQDSQVIVTGNLIDISTELGNVANSISNALDK 480
DB 421 RHSCNVLSLDGITLRLSGEFDAAQYKNVSIILNSQVIVTGNLIDISTELGNVANSISNALNK 480
QY 481 LEENSCKLDKVNKLTSTLSALITYIVLTIVISLVCGLSLVLAACYLMHKQKQAKQKTLMLG 540
DB 481 LEENSCKLDKVNRLTNTSALITYIVLTIVISLVCGLSLVLAACYLMHKQKQAKQKTLMLG 540
QY 541 NNTLDQMRATTK 552
DB 541 NNTLDQMRATTK 552
RESULT 13
VGLF SV5
ID VGLF SV5 STANDARD; PRT; 529 AA.
AC P04849;
DT 13-AUG-1987 (Rel. 05, Created)
DT 13-AUG-1987 (Rel. 05, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Fusion glycoprotein precursor [Contains: Fusion glycoprotein F2;
DE Fusion glycoprotein F1].
GN F.
OS Simian virus 5 (strain W3) (SV5).
OC Viruses; ssRNA negative-strand viruses; Mononegavirales;
OC Paramyxoviridae; Paramyxovirinae; Rubulavirus.
OX NCBI_TaxID=11208;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=85038582; PubMed=6093114;
RA Paterson R.G., Harris T.J.R., Lamb R.A.;
RT "Fusion protein of the paramyxovirus simian virus 5: nucleotide
RT sequence of mRNA predicts a highly hydrophobic glycoprotein.";
RN [2]
RN Proc. Natl. Acad. Sci. U.S.A. 81:6706-6710(1984).
RP X-RAY CRYSTALLOGRAPHY (1.4 ANGSTROMS) OF 122-185 AND 440-477.
RX MEDLINE=99214846; PubMed=10198633;
RA Baker K.A., Dutch R.E., Lamb R.A., Jardetzky T.S.;
RT "Structural basis for paramyxovirus-mediated membrane fusion.";
RL Mol. Cell 3:309-319(1999).
CC -!- FUNCTION: This protein directs fusion of viral and cellular
CC membranes.
CC -!- SUBUNIT: THE MATURE FORM IS A DIMER OF POLYPEPTIDES F-1 AND F-2
CC LINKED BY A DISULFIDE BOND.
CC -!- SIMILARITY: Belongs to the paramyxoviruses fusion glycoprotein
CC family.
CC
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CC
CC EMBL; K02253; AAA47881.1; -;
CC EMBL; AF052755; AAC95515.1; -;
CC PIR; A21688; VGNZSP.
CC PDB; 1SVF; 26-MAR-99.
CC InterPro; IPR000776; Fusion gly.
CC Pfam; PF00523; fusion gly; 1.

Glycoprotein; Fusion protein; Transmembrane; Envelope protein; Signal; 3D-structure.

1 19 FUSION GLYCOPROTEIN F0.
 20 529 F2 PROTEIN.
 21 102 F1 PROTEIN.
 22 103 LINKAGE BETWEEN F2 & F1 (POTENTIAL).
 23 529 LINKAGE BETWEEN F2 & F1 (POTENTIAL).
 24 64 N-LINKED (GLCNAC. . .) (POTENTIAL).
 25 65 N-LINKED (GLCNAC. . .) (POTENTIAL).
 26 73 N-LINKED (GLCNAC. . .) (POTENTIAL).
 27 352 N-LINKED (GLCNAC. . .) (POTENTIAL).
 28 427 N-LINKED (GLCNAC. . .) (POTENTIAL).
 29 431 N-LINKED (GLCNAC. . .) (POTENTIAL).
 30 457 N-LINKED (GLCNAC. . .) (POTENTIAL).
 31 174 N-LINKED (GLCNAC. . .) (POTENTIAL).
 32 175
 33 176
 34 182
 35 184
 36 450
 37 475
 38 476
 39 476

SEQUENCE 529 AA; 56597 MW; 3152C37B1A8A2C7E CRC64;
 Query Match 26.0%; Score 717; DB 1; Length 529;
 Best Local Similarity 34.8%; Pred. No. 2e-37;
 Matches 179; Conservative 89; Mismatches 233; Indels 14; Gaps 6;

14 MLTVRVALASC-VCPNSSLDGRPLAAAGIVTGDKAVNIYTSSTQSGSIIVKLLPNPKD 72
 1 MGTHIQFLVSCLLAGAGSLDPAALMQIVTPTNVRQLMYITEASSAFIVVKLLPMTDSP 60
 73 KEACAKAPLEAYNRTLTLLTPLGDSIRRIQESVTTSGGKGQRLIGALIGGAALGATA 132
 61 ISGCNITSISSYNATVTKLQPIGENLETIRNQLIPT--RRRRFAGVWIGLAALGATA 118
 133 AQITTAASALIQANQANANILRLKERIAATNEAVHEVTDGLSQLAVAGKMQQFVNDQFNK 192
 119 AQVTAASALVAVKANENAAAILNKNAIQKTAANAADVVQATQSLGTAVQAVQDHINSVVSP 178
 193 TAQELDCIKITQOVGVVELNLYLTTLTVPFGPQITSPALTOITQALYNLAGNMDYLLTK 252
 179 AITAAKQADAIIGTILNLYLTTLTIFHNQITNPALSPITQALRILGSTLPTVVEK 238
 253 LGVGNQLSS--LIGSGLTGNPILYDSQTLGIGIQTLPVSGNLMNRATYLETLLSVST 310
 239 --SFNTQISAEILLSGLLTGQIVGLDLYNQWIKIELPTLTVPQATQIDLATISAFI 296
 311 TKGFASALVPKVMKGVSVIEELDTSYCIETDLDLYCTRIVTFPMSPGIYSCLSGNTSAC 370
 297 NNOEVWAQLPRTVMVTGSLIQAVPASQCTITPTNTVYCRYNDAQVLSDDTMACLQGNLTRC 356
 371 MYSTEGALTPTMYTLKGSVIANCKMTTCRCADPPGIISQNYGEAVSLIDRQSCNVLSLD 430
 357 TFSFVGSFTRFVLFPGIYVANCRCMLCKMQPAVILQPSPPSVPTVIDMYKCVSLQLD 416
 431 GITRLSGEEDATYQKNISIQDSQVIVTGNLIDISTELGNVNNISNALDKLEBSNKLDK 490
 417 NLRFTITQLANVTYNSPIKLESSQILSIDPDISQNLAAVKNKSLSDALQHLAQSDTYLSA 476
 491 VNVKLTSTALITYIVTLTVSLVCGILSVIACVL 525
 477 I-----TSATTT--SVLSIIAICLGLSLILIL 504

RESULT 14
 VGLF_MUMPM STANDARD; PRT; 538 AA.
 AC P11236;
 DT 01-JUL-1989 (Rel. 11, Created)
 DT 01-JUL-1989 (Rel. 11, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Fusion glycoprotein precursor [Contains: Fusion glycoprotein F2;
 GN Fusion glycoprotein F1].
 OS Mumps virus (strain Miyahara vaccine).

Viruses; ssRNA negative-strand viruses; Mononegavirales;
 Paramyxoviridae; Paramyxovirinae; Rubulavirus.
 NCBI_TaxID=11171;
 [1]
 SEQUENCE FROM N.A.
 MEDLINE=89345174; PubMed=2762156;
 Takeuchi K., Tanahayashi K., Hishiyama M., Yamada A., Sugiura A.;
 "Cloning and sequencing of the fusion protein gene of mumps virus
 (Miyahara strain).";
 Nucleic Acids Res. 17:5839-5839(1989).
 !- FUNCTION: This protein directs fusion of viral and cellular
 membranes.
 !- SUBUNIT: THE MATURE FORM IS A DIMER OF POLYPEPTIDES F-1 AND F-2
 !- LINKED BY A DISULFIDE BOND.
 !- SIMILARITY: Belongs to the paramyxoviruses fusion glycoprotein
 family.

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 EMBL; X15285; CAA33359.1; -;
 DR A34062; VGNZMM.
 DR HSPP; P04849; ISVF.
 DR InterPro; IPR000776; Fusion gly.
 DR Pfam; PF00523; fusion gly. 1;
 Glycoprotein; Fusion protein; Transmembrane; Envelope protein; Signal.
 SIGNAL 1 19
 FT CHAIN 20 538 FUSION GLYCOPROTEIN F0.
 FT CHAIN 20 97 F2 PROTEIN.
 FT CHAIN 103 538 F1 PROTEIN.
 FT TRANSMEM 483 512 POTENTIAL.
 FT DISULFID 64 185 LINKAGE BETWEEN F2 & F1 (POTENTIAL).
 FT CARBOHYD 73 173 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 182 182 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 352 352 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 427 427 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 433 433 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 457 457 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 538 AA; 58711 MW; C2589DE46C40F67 CRC64;
 Query Match 25.8%; Score 712.5; DB 1; Length 538;
 Best Local Similarity 33.1%; Pred. No. 4e-37;
 Matches 171; Conservative 108; Mismatches 220; Indels 17; Gaps 7;

13 MLTVRVALASCVCPTSSSLDGRPLAAAGIVTGDKAVNIYTSSTQSGSIIVKLLPNPKD 72
 5 LVTCLGFAVFSVSSVCVNINI---LQIGIKQVRLSYSSQSSSYIVVKLLPNQPT 60
 73 KEACAKAPLEAYNRTLTLLTPLGDSIRRIQESVTTSGGKGQRLIGALIGGAALGATA 132
 61 DSCPEKSVTYQYKTLNLLPLPAENINNI--ASPSGSRHRKRFAGIALIGALGATA 118
 133 AQITTAASALIQANQANANILRLKERIAATNEAVHEVTDGLSQLAVAGKMQQFVNDQFNK 192
 119 AQVTAASALVAVQATNARATAAMKNSIQATNRAVFEVKEGTQRLAIAVQAIQDHINTIMT 178
 193 TAQELDCIKITQOVGVVELNLYLTTLTVPFGPQITSPALTOITQALYNLAGNMDYLLTK 252
 179 QLNMSQCILDNDQLATSLGLYLTTLTVPQQLINPALSPISITQALRSLIGSMTPAVQA 238
 253 LGVGNQLSSLIGSLITGN--PILYDSQTLGIGIQTLPVSGNLMNRATYLETLLSVST 310
 239 TLSTSIASAEILLSAGLMGQIVSVLDEMQMI--VKINIPITVITQSN--ALVIDFYSISS 294
 311 TKGFASALV--PKVVMKGVSVIEELDTSYCIETDLDLYCTRIVTFPMSPGIYSCLSGNTS 368
 295 FINNQESIQLPDRILEIGNEQWSPAKNCKLRRHIFCQYNEAERLSLESKLCLAGNIS 354

QY 369 ACMSKTEGALTTPYMTLKGSIANCKMTTCRCADPPGIISQNYGEAVSLIDROSCNVLS 428
Db 355 ACVSPAGSYMRFEALDGIIVANCRSLTCLCKSPSPYIQPDHATVITDLACQTLIS 414
QY 429 LGITRLSGDFDQATYQKNIQSDQSVITGNLDISTELGNVNNISNALDKLEESNKL 488
Db 415 LDGLDFSVLSNITYAENLATSISQNTQPIDISTELSKVNASLQNAVYIKESNHL 474
QY 489 DKVNVKLTSTALITYIVITVLSVCGILSLVLA 524
Db 475 QSVNNSKIGAITVAALVLSLSI---IISLFCWC 507

RESULT 15

VCLF P12H STANDARD; PRT; 551 AA.
AC P25467;
DT 01-MAY-1992 (Rel. 22, Created)
DT 01-MAY-1992 (Rel. 22, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Fusion glycoprotein precursor (Contains: Fusion glycoprotein F2;
Fusion glycoprotein F1).
GN F.
OS Human parainfluenza 2 virus (PIV-2).
OC Viruses; ssRNA negative-strand viruses; Mononegavirales;
OC Paramyxoviridae; Paramyxovirinae; Rubulavirus.
OX NCBI_TaxID=11212;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=91049467; PubMed=2173268;
RA Hu X., Compans R.W., Matsuoaka Y., Ray R.;
RT "Molecular cloning and sequence analysis of the fusion glycoprotein
RT gene of human parainfluenza virus type 2.";
RL Virology 179:915-920(1990).
CC -!- FUNCTION: This protein directs fusion of viral and cellular
CC membranes.
CC -!- SUBUNIT: THE MATURE FORM IS A DIMER OF POLYPEPTIDES F-1 AND F-2
CC LINKED BY A DISULFIDE BOND.
CC -!- SIMILARITY: Belongs to the paramyxoviruses fusion glycoprotein
CC family.
CC

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DR EMBL; M60182; AAA46843.1; -.
DR HSSP; P04849; 1SVF.
DR InterPro; IPR000776; Fusion gly.
DR Pfam; PF00523; fusion_gly; 1.
KW Glycoprotein; Fusion protein; Transmembrane; Envelope protein; Signal.
FT SIGNAL 1 25
FT CHAIN 26 551
FT CHAIN 26 106
FT CHAIN 107 551
FT TRANSMEM 107 132
FT TRANSMEM 486 513
FT DISULFID 68 189
FT CARBOHYD 65 65
FT CARBOHYD 69 69
FT CARBOHYD 77 77
FT CARBOHYD 90 90
FT CARBOHYD 431 461
FT CARBOHYD 461 461
SQ SEQUENCE 551 AA; 59668 MW; 0003A2635A3AA0C8 CRC64;

Query Match 25.6%; Score 706; DB 1; Length 551;

Best Local Similarity 33.2%; Pred. No. 1e-36; Mismatches 217; Indels 10; Gaps 6;

QY 29 TSSLDGRPLAAGIIVTGDKAVNIYTSSQTGSIIVKLLPNMPKDEACAKAFLEAYNRTL 88
Db 21 SDATAGDQLLNGIVGSIKIRSLMYTDDGASFIWVKLLPNLPSPNGTNIITSLDAYNVTL 80
QY 89 TTLTLPGLDSIRRIQESVTTSGGKGQRLIGAIIGGAALGVATAAQITAAASALIOANQNA 148
Db 81 FKLLTFLIENLSKI--STVTDTKTRKRFAGVWVGLAALGVATAAQITAAVAIVKANANA 138
QY 149 ANILRLKERIAATNEAVHEVTDGLSOLAVAVKMQQFVNDQFNKTAQELDCIKITQQQGV 208
Db 139 AAINNLAASSIQSTNKAVSDVIDASRTIATAVQAIQDHINGAIVNGITSASCRADHALLGS 198
QY 209 ELNLYLTETTVFGPQITSPALTOLTIQALYNLAGNMDYLL-TKLGVGNLSSLIGSG 267
Db 199 IINLYLTETTVFHNQITNPALTPLISQALLILGSTLPIVIESKLT-NLNTALLSG 257
QY 268 LITGNPILYDSQTQLLGIQVTLPSVGNLNNRATYLETSLVSTTKGFASAL--VPKVMK 325
Db 258 LLTGQIISISPMYMQMLIQINVPTF--LMQPGAKVIDLIAISANHKLOEVVVVQVNPRIE 315
QY 326 VGSVIEELDTSYCIETDLDLCTRIVTTPMSPGIYSCLSGNTSACMYSKTEGALTTPYMT 385
Db 316 YANELQNPANDCVVTPNSVFCRYNEGSPIPESQYQCLRGNLNSCTFTPIIGNFLKRF 375
QY 386 LKGSVIANCKMTTCRCADPPGIISQNYGEAVSLIDROSCNVLSLDGITRLSGEDATVQ 445
Db 376 ANGVLYANCKSLLCRCADPPHVVSQDDTQGISIIDIKCESEMMLDTFSFRITSTENATV 435
QY 446 KNISIQDSQVITVGNLDISTELGNVNNISNALDKLEESNKLDKVNVKLTSTALITYI 505
Db 436 TDFSMINANIVHLSPLDLSNQINSINKSLKAEDWIADSNFFANQARTAKTIYLSLATAL 495
QY 506 VLTWISLVCGILSLVLA 522
Db 496 ILSVITLV--VWGLLIA 510

Search completed: April 18, 2004, 01:07:20

Job time : 42 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: April 18, 2004, 01:07:24 ; Search time 84 Seconds
(without alignments)
2077.161 Million cell updates/sec

Title: US-10-725-841-2
Perfect score: 2757
Sequence: 1 MGSRSSTRIPVPLMLTVRA.....KTLWLGNNTLDQMRATTKM 553

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL 25:*
1: sp archaea:*
2: sp bacteria:*
3: sp fungi:*
4: sp human:*
5: sp invertebrate:*
6: sp mammal:*
7: sp mhc:*
8: sp organelle:*
9: sp phage:*
10: sp plant:*
11: sp rodent:*
12: sp virus:*
13: sp vertebrate:*
14: sp unclassified:*
15: sp_rvirus:*
16: sp_bacteriap:*
17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	2716	98.5	553	12	Q9J1C8
2	2658	96.4	553	12	Q83855
3	2623	95.1	553	12	Q7T6W0
4	2621	95.1	551	12	Q8QT25
5	2621	95.1	551	12	Q8V1Q7
6	2621	95.1	551	12	Q8QT13
7	2621	95.1	553	12	Q80KD0
8	2619	95.0	553	12	Q9WMH7
9	2616	94.9	553	12	Q90339
10	2615	94.8	553	12	Q91AH8
11	2612	94.7	551	12	Q8QT12
12	2611	94.7	553	12	Q9WLE2
13	2606	94.5	553	12	Q9WLE1
14	2605	94.5	553	12	Q9WD11
15	2605	94.5	553	12	Q91HX4
16	2605	94.5	553	12	Q9WN22

17	2605	94.5	553	12	Q9DLD4	Q9DLD4 newcastle d
18	2602	94.4	553	12	Q83849	Q83849 newcastle d
19	2599	94.3	553	12	O90362	O90362 newcastle d
20	2584	93.7	551	12	Q8QT22	Q8QT22 newcastle d
21	2575	93.4	553	12	Q83854	Q83854 newcastle d
22	2572	93.3	551	12	Q8QT23	Q8QT23 newcastle d
23	2556	92.7	551	12	Q8QT21	Q8QT21 newcastle d
24	2556	92.7	551	12	Q8QT15	Q8QT15 newcastle d
25	2554	92.6	551	12	Q8QT18	Q8QT18 newcastle d
26	2554	92.6	553	12	O92150	O92150 newcastle d
27	2553	92.6	551	12	Q8QT19	Q8QT19 newcastle d
28	2552	92.6	553	12	O9WF46	O9WF46 newcastle d
29	2549	92.5	553	12	O91AP6	O91AP6 newcastle d
30	2543	92.5	553	12	Q83856	Q83856 newcastle d
31	2548	92.4	551	12	Q8QT16	Q8QT16 newcastle d
32	2547	92.4	551	12	Q8QT17	Q8QT17 newcastle d
33	2547	92.4	553	12	Q83847	Q83847 newcastle d
34	2544	92.3	551	12	Q8QT20	Q8QT20 newcastle d
35	2542	92.2	553	12	O91HX3	O91HX3 newcastle d
36	2541	92.2	551	12	Q8V1Q0	Q8V1Q0 newcastle d
37	2540	92.1	551	12	O8V1Q2	O8V1Q2 newcastle d
38	2538	92.1	551	12	O8V1Q5	O8V1Q5 newcastle d
39	2537	92.0	553	12	O914E7	O914E7 newcastle d
40	2536	92.0	553	12	O56771	O56771 newcastle d
41	2536	92.0	553	12	O9QPS2	O9QPS2 newcastle d
42	2536	92.0	553	12	O7T7T3	O7T7T3 goose param
43	2535	91.9	551	12	Q8QT24	Q8QT24 newcastle d
44	2532	91.8	551	12	O91AL4	O91AL4 newcastle d
45	2531	91.8	553	12	Q9WI28	Q9WI28 newcastle d

ALIGNMENTS

RESULT 1

Q9J1C8 PRELIMINARY; PRT; 553 AA.
AC Q9J1C8
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Fusion protein.
OS Newcastle disease virus.
OC Viruses; ssRNA negative-strand viruses; Mononegavirales;
OC Paramyxoviridae; Paramyxovirinae; Rubulavirus.
OX NCBI_TaxID=11176;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Queensland.
RA Chen L., Colman P.M., Gorman J.J.;
RT "Nucleotide sequence of the fusion protein of V4 isolate of the
RT Queensland strain of Newcastle disease virus.";
RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF217084; AAF42837.1; -
DR PIR; S23621.
DR GO; GO:0019039; F:Viral-cell fusion molecule activity; IEA.
DR GO; GO:0006948; P:Viral-induced cell-cell fusion; IEA.
DR InterPro; IPR000776; Fusion_gly.
DR Pfam; PF00523; fusion_gly; 1.
SQ SEQUENCE 553 AA; 56843 MW; 0535FFB293FF897E CRC64;

Query Match 98.5%; Score 2716; DB 12; Length 553;
Best Local Similarity 98.2%; Pred. No. 3.2e-167;
Matches 543; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

QY 1 MGSRSSTRIPVPLMLTVRAALSCVCPSSLDGRPLAAGIVTGDKAVNIYTSQTGS 60

Db 1 MGSRSSTRIPVPLMLTVRAALSCVCPSSLDGRPLAAGIVTGDKAVNIYTSQTGS 60

QY 61 IIVKLLPNMPKOEACAKAPLEAYNRTLTLLTPLGDSIRRIQESVTTSGGKQGRLLGA 120

Db 61 IIVKLLPNMPKOEACAKAPLEAYNRTLTLLTPLGDSIRRIQESVTTSGGKQGRLLGA 120

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QY 121 IIGGAALGVATAAQTAAASALIQANONAAANILRLKERIAATNEAVHEVTGDSQLAVAVG 180
DB 121 IIGGVALGVATAAQTAAASALIQANONAAANILRLKESIAATNEAVHEVTGDSQLAVAVG 180
QY 181 KMQQFVNDQFNKTAQELDCIKITQQGVVELNLYLTELTTVFPGQITSPALTIQALYN 240
DB 181 KMQQFVNDQFNKTAQELDCIKITQQGVVELNLYLTELTTVFPGQITSPALTIQALYN 240
QY 241 LAGGNDYLLTKLGVGNQSLIGSLITGNPILYDSQTQLLGLQVTLPSVGNLNNMRA 300
DB 241 LAGGNDYLLTKLGVGNQSLIGSLITGNPILYDSQTQLLGLQVTLPSVGNLNNMRA 300
QY 301 TYLETSLVSTTKGFASALVPKVMKGVSVIEELDTSYCIETDLDLYCTRIVTFPMSPGIY 360
DB 301 TYLETSLVSTTKGFASALVPKVMKGVSVIEELDTSYCIETDLDLYCTRIVTFPMSPGIY 360
QY 361 SCLSGNTSACMYSTEGALTPPYMTLKGSVIANCKMTTCRCADPPGIIISQNYGEAVSLID 420
DB 361 SCLSGNTSACMYSTEGALTPPYMTLKGSVIANCKMTTCRCADPPGIIISQNYGEAVSLID 420
QY 421 ROSCNVLSLDGITLRLSGEFDATYQKNISIODSQVIVTGNLIDISTELGNVNNISNALDK 480
DB 421 ROSCNVLSLDGITLRLSGEFDATYQKNISIODSQVIVTGNLIDISTELGNVNNISNALDK 480
QY 481 LEESNKLDKVNKLTSTSAITYIVLTVISLVCGLISLVACYLMYKQKQKQKTLMLG 540
DB 481 LEESNKLDKVNKLTSTSAITYIVLTVISLVCGLISLVACYLMYKQKQKQKTLMLG 540
QY 541 NNTLDQMRATTKM 553
DB 541 NNTLDQMRATTKM 553

RESULT 2
Q83855 PRELIMINARY; PRT; 553 AA.
AC Q83855;
DT 01-NOV-1996 (TremBLrel. 01, Created)
DT 01-NOV-1996 (TremBLrel. 01, Last sequence update)
DT 01-OCT-2003 (TremBLrel. 25, Last annotation update)
DE F protein.
OS Newcastle disease virus.
OC Viruses; ssRNA negative-strand viruses; Mononegavirales;
OC Paramyxoviridae; Paramyxovirinae; Rubulavirus.
OX NCBI_TaxID=11176;
RN [1]_TaxID=11176;
RP SEQUENCE FROM N.A.
RC STRAIN=Ulster mutant;
RX MEDLINE=90261333; PubMed=2188464;
RA Pritzer E., Kuroda K., Garten W., Nagai Y., Klenk H.P.;
RT "A host range mutant of Newcastle disease virus with an altered
RT cleavage site for proteolytic activation of the F protein.";
RL Virus Res. 15:237-242(1990).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=Ulster mutant;
RA Garten W.D.;
RL Submitted (MAY-1992) to the EMBL/GenBank/DBJ databases.
DR EMBL; 212110; CA478095.1; -.
DR PIR; S23621; S23621.
DR PIR; S38785; S38785.
DR GO; GO:0009573; C:ribulose biphosphate carboxylase complex; IEA.
DR GO; GO:0016984; F:ribulose-biphosphate carboxylase activity; IEA.
DR GO; GO:0019039; F:viral-cell fusion molecule activity; IEA.
DR GO; GO:0015977; F:carbon utilization by fixation of carbon di. . .; IEA.
DR GO; GO:0006946; F:viral-induced cell-cell fusion; IEA.
DR InterPro; IPR000776; Fusion Gly.
DR InterPro; IPR000685; Rubisco large.
DR Pfam; PF00523; fusion gly; 1.
SQ SEQUENCE 553 AA; 5899 MW; D478EA1A51A6BADE8 CRC64;

Query Match 96.4%; Score 2658; DB 12; Length 553;
Best Local Similarity 96.9%; Pred. No. 1.8e-163;
Matches 524; Conservative 11; Mismatches 18; Indels 0; Gaps 0;
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Matches 536; Conservative 2; Mismatches 15; Indels 0; Gaps 0;
QY 1 MGSRSSTRIPVPLMLTVRVALALSCVCPSTSLDGRPLAAAGIVVTGDKAVNIYTSSTQGS 60
DB 1 MGSRSSTRIPVPLMLTVRVALALSCVCPSTSLDGRPLAAAGIVVTGDKAVNIYTSSTQGS 60
QY 61 IIVKLLPNMPKDEACAKAPLEAVNRTLTLLTPLGDSIRRIQBSVTTSGGKQRLIGA 120
DB 61 IIVKLLPNMPKDEACAKAPLEAVNRTLTLLTPLGDSIRRIQBSVTTSGGKQRLIGA 120
QY 121 IIGGAALGVATAAQTAAASALIQANONAAANILRLKERIAATNEAVHEVTGDSQLAVAVG 180
DB 121 IIGGVALGVATAAQTAAASALIQANONAAANILRLKESIAATNEAVHEVTGDSQLAVAVG 180
QY 181 KMQQFVNDQFNKTAQELDCIKITQQGVVELNLYLTELTTVFPGQITSPALTIQALYN 240
DB 181 KMQQFVNDQFNKTAQELDCIKITQQGVVELNLYLTELTTVFPGQITSPALTIQALYN 240
QY 241 LAGGNDYLLTKLGVGNQSLIGSLITGNPILYDSQTQLLGLQVTLPSVGNLNNMRA 300
DB 241 LAGGNDYLLTKLGVGNQSLIGSLITGNPILYDSQTQLLGLQVTLPSVGNLNNMRA 300
QY 301 TYLETSLVSTTKGFASALVPKVMKGVSVIEELDTSYCIETDLDLYCTRIVTFPMSPGIY 360
DB 301 TYLETSLVSTTKGFASALVPKVMKGVSVIEELDTSYCIETDLDLYCTRIVTFPMSPGIY 360
QY 361 SCLSGNTSACMYSTEGALTPPYMTLKGSVIANCKMTTCRCADPPGIIISQNYGEAVSLID 420
DB 361 SCLSGNTSACMYSTEGALTPPYMTLKGSVIANCKMTTCRCADPPGIIISQNYGEAVSLID 420
QY 421 ROSCNVLSLDGITLRLSGEFDATYQKNISIODSQVIVTGNLIDISTELGNVNNISNALDK 480
DB 421 ROSCNVLSLDGITLRLSGEFDATYQKNISIODSQVIVTGNLIDISTELGNVNNISNALDK 480
QY 481 LEESNKLDKVNKLTSTSAITYIVLTVISLVCGLISLVACYLMYKQKQKQKTLMLG 540
DB 481 LEESNKLDKVNKLTSTSAITYIVLTVISLVCGLISLVACYLMYKQKQKQKTLMLG 540
QY 541 NNTLDQMRATTKM 553
DB 541 NNTLDQMRATTKM 553

RESULT 3
Q7T6W0 PRELIMINARY; PRT; 553 AA.
AC Q7T6W0;
DT 01-OCT-2003 (TremBLrel. 25, Created)
DT 01-OCT-2003 (TremBLrel. 25, Last sequence update)
DT 01-OCT-2003 (TremBLrel. 25, Last annotation update)
DE Fusion protein.
OS Newcastle disease virus.
OC Viruses; ssRNA negative-strand viruses; Mononegavirales;
OC Paramyxoviridae; Paramyxovirinae; Rubulavirus.
OX NCBI_TaxID=11176;
RN [1]_TaxID=11176;
RP SEQUENCE FROM N.A.
RC STRAIN=Luoyi;
RA Hu R., Bao S., Zhang S.;
RT "Molecular epidemiological investigation of different strains of
RT Newcastle disease virus.";
RL Submitted (JUL-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY341061; AAQ16124.1; -.
SQ SEQUENCE 553 AA; 59016 MW; 20F113CEE2D9E194 CRC64;

Query Match 95.1%; Score 2623; DB 12; Length 553;
Best Local Similarity 94.8%; Pred. No. 3.3e-161;
Matches 524; Conservative 11; Mismatches 18; Indels 0; Gaps 0;
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QY 1 MGSRSSTRIPVPLMLTVRVALALSCVCPSTSLDGRPLAAAGIVVTGDKAVNIYTSSTQGS 60
DB 1 MGPKSSTNVPAPLMLTVRIALALSCVRLTNSLDGRPLAAAGIVVTGDKAVNIYTSSTQGS 60
```

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QY 61 IIVKLLPNPKDKEACAKAPLEAYNRTLTLLTPLGDSIRRIQESVTTSGGKQGRLLGA 120
DB 61 IIVKLLPNPKDKEACAKAPLEAYNRTLTLLTPLGDSIRRIQESVTTSGGKQGRFFGA 120
QY 121 IIGGAALGVATAAQITAAASALIQANQNAANILRLKERIAATNEAVHEVTDGLSOLAVAVG 180
DB 121 IIGSVALGVATAAQITAAASALIQANQNAANILRLKESIAATNEAVHEVTDGLSOLAVAVG 180
QY 181 KMQQFVNDQFNKTAQELDCIKITQQVGVVELNLYLTETTTVFGPQITSPALTIQALYN 240
DB 181 KMQQFVNDQFNNTAQELDCIKITQQVGVVELNLYLTETTTVFGPQITSPALTIQALYN 240
QY 241 LAGNNMDYLLTKLGVGNQNLSSLIGSLITGNPILYDSOTQLLGIQVTLPSVGNLNMRA 300
DB 241 LAGNNMDYLLTKLGVGNQNLSSLIGSLITGNPILYDSOTQLLGIQVTLPSVGNLNMRA 300
QY 301 TYLETLSVSTTKGFASALVPKVMKGVSVIEELDTSCYIETDLDLYCTRIIVTFPMSPGIY 360
DB 301 TYLETLSVSTTKGFASALVPKVMKGVSVIEELDTSCYIETDLDLYCTRIIVTFPMSPGIY 360
QY 361 SCLSGNTSACMYKTEGALTTPYMTIKGVIANKMTTCRCADPPGHIISQNYGEAVSLID 420
DB 361 SCLSGNTSACMYKTEGALTTPYMTIKGVIANKMTTCRCADPPGHIISQNYGEAVSLID 420
QY 421 ROSCNVLSLDGITLRLSGEFDATYQKNISIQDSQVIVTGNLDISTELGNVNNISNALDK 480
DB 421 RHSCNVLSLDGITLRLSGEFDATYQKNISIQDSQVIVTGNLDISTELGNVNNISNALDK 480
QY 481 LEEESKLDKVNKLTSTSLIYIVLTVISLVCGLISLVACYLVMYKQAKQKTLILWL 540
DB 481 LEEESKLDKVNKLTSTSLIYIVLTVISLVCGLISLVACYLVMYKQAKQKTLILWL 540
QY 541 NNTLDQWRATT 551
DB 541 NNTLDQWRATT 551
```

RESULT 4

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ID Q8Q725 PRELIMINARY; PRT; 551 AA.
AC Q8Q725;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Fusion protein (Fragment).
OS Newcastle disease virus.
OC Viruses; ssRNA negative-strand viruses; Mononegavirales;
OC Paramyxoviridae; Paramyxovirinae; Rubulavirus.
OX NCBI_TaxID=11176;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=FJ-1/85;
RA Ni X., Wu Y., Liu X.;
RT "Molecular epizootiological study of chicken Newcastle disease (ND) in
RT east China."
RL Zhongguo jiaqin 0:0-0(2002).
DR EMBL; AF458009; AML3424.1; -.
DR GO; GO:0019039; F:Viral-cell fusion molecule activity; IEA.
DR GO; GO:0006948; P:Viral-induced cell-cell fusion; IEA.
DR InterPro; IPR000776; Fusion gly.
DR Pfam; PF00523; fusion gly; I.
FT NON_TER 551
SQ SEQUENCE 551 AA; 58730 MW; 93CE2D9E1947BFA CRC64;
```

Query Match 95.1%; Score 2621; DB 12; Length 551;
Best Local Similarity 95.1%; Pred. No. 4.4e-161;
Matches 524; Conservative 9; Mismatches 18; Indels 0; Gaps 0;

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QY 1 MGRSSTRIPVPLMLTVRVALALSCVCPSTSLDGRPLAAAGIVVTGDKAVNIYTSQTGS 60
DB 1 MGPKSTNVPAFLMLTVRIALALSCVRLTNSLDGRPLAAAGIVVTGDKAVNIYTSQTGS 60
QY 61 IIVKLLPNPKDKEACAKAPLEAYNRTLTLLTPLGDSIRRIQESVTTSGGKQGRLLGA 120
```

```
DB 61 IIVKLLPNPKDKEACAKAPLEAYNRTLTLLTPLGDSIRRIQESVTTSGGKQGRFFGA 120
QY 121 IIGGAALGVATAAQITAAASALIQANQNAANILRLKERIAATNEAVHEVTDGLSOLAVAVG 180
DB 121 IIGSVALGVATAAQITAAASALIQANQNAANILRLKESIAATNEAVHEVTDGLSOLAVAVG 180
QY 181 KMQQFVNDQFNKTAQELDCIKITQQVGVVELNLYLTETTTVFGPQITSPALTIQALYN 240
DB 181 KMQQFVNDQFNNTAQELDCIKITQQVGVVELNLYLTETTTVFGPQITSPALTIQALYN 240
QY 241 LAGNNMDYLLTKLGVGNQNLSSLIGSLITGNPILYDSOTQLLGIQVTLPSVGNLNMRA 300
DB 241 LAGNNMDYLLTKLGVGNQNLSSLIGSLITGNPILYDSOTQLLGIQVTLPSVGNLNMRA 300
QY 301 TYLETLSVSTTKGFASALVPKVMKGVSVIEELDTSCYIETDLDLYCTRIIVTFPMSPGIY 360
DB 301 TYLETLSVSTTKGFASALVPKVMKGVSVIEELDTSCYIETDLDLYCTRIIVTFPMSPGIY 360
QY 361 SCLSGNTSACMYKTEGALTTPYMTIKGVIANKMTTCRCADPPGHIISQNYGEAVSLID 420
DB 361 SCLSGNTSACMYKTEGALTTPYMTIKGVIANKMTTCRCADPPGHIISQNYGEAVSLID 420
QY 421 ROSCNVLSLDGITLRLSGEFDATYQKNISIQDSQVIVTGNLDISTELGNVNNISNALDK 480
DB 421 RHSCNVLSLDGITLRLSGEFDATYQKNISIQDSQVIVTGNLDISTELGNVNNISNALDK 480
QY 481 LEEESKLDKVNKLTSTSLIYIVLTVISLVCGLISLVACYLVMYKQAKQKTLILWL 540
DB 481 LEEESKLDKVNKLTSTSLIYIVLTVISLVCGLISLVACYLVMYKQAKQKTLILWL 540
QY 541 NNTLDQWRATT 551
DB 541 NNTLDQWRATT 551
```

RESULT 5

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ID Q8V1Q7 PRELIMINARY; PRT; 551 AA.
AC Q8V1Q7;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Fusion protein (Fragment).
GN F.
OS Newcastle disease virus.
OC Viruses; ssRNA negative-strand viruses; Mononegavirales;
OC Paramyxoviridae; Paramyxovirinae; Rubulavirus.
OX NCBI_TaxID=11176;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=JS/1/97/Go;
RA Wan H., Wu Y., Liu X., Zhang R.;
RT "Sequence analysis of the fusion (F) protein genes of four Newcastle
RT disease virus strains causing clinical disease in geese."
RL Wei Sheng Wu Heuh Pao 0:0-0(2002).
DR EMBL; AF456435; AAL57897.1; -.
DR GO; GO:0019039; F:Viral-cell fusion molecule activity; IEA.
DR GO; GO:0006948; P:Viral-induced cell-cell fusion; IEA.
DR InterPro; IPR000776; Fusion gly.
DR Pfam; PF00523; fusion gly; I.
FT NON_TER 551
SQ SEQUENCE 551 AA; 58730 MW; 93CE2D9E1947BFA CRC64;
```

Query Match 95.1%; Score 2621; DB 12; Length 551;
Best Local Similarity 95.1%; Pred. No. 4.4e-161;
Matches 524; Conservative 9; Mismatches 18; Indels 0; Gaps 0;

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QY 1 MGRSSTRIPVPLMLTVRVALALSCVCPSTSLDGRPLAAAGIVVTGDKAVNIYTSQTGS 60
DB 1 MGPKSTNVPAFLMLTVRIALALSCVRLTNSLDGRPLAAAGIVVTGDKAVNIYTSQTGS 60
QY 61 IIVKLLPNPKDKEACAKAPLEAYNRTLTLLTPLGDSIRRIQESVTTSGGKQGRLLGA 120
```

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Db 11VXLLPNPKDKEACAPLEAYNRTLTLLTPLGDSIRRIQESATTSGGRRQRFICA 120
QY 121 IIGGAALGVATAAQITTAASALIQAQNAANILRLKERIAATNEAVHEVTDGLSOLAVAG 180
Db 121 IIGSVLGVATAAQITTAASALIQAQNAANILRLKERIAATNEAVHEVTDGLSOLAVAG 180
QY 181 KMOQFVNDQFNKTAQELDCIKITQOVGVNELNYLTTELTTVFGPQITSPALTIQALYN 240
Db 181 KMOQFVNDQFNKTAQELDCIKITQOVGVNELNYLTTELTTVFGPQITSPALTIQALYN 240
QY 241 LAGNMDYLLTKLGVGNQSLIGSLITGNPIYDSOTQLLGIQVTLPSVGNLNNMRA 300
Db 241 LAGNMDYLLTKLGVGNQSLIGSLITGNPIYDSOTQLLGIQVTLPSVGNLNNMRA 300
QY 301 TYLETSLVSTTKGFASALVPKVMKGVSVBELDTSYCIETDLDLYCTRIVTFPMSPGIY 360
Db 301 TYLETSLVSTTKGFASALVPKVMKGVSVBELDTSYCIETDLDLYCTRIVTFPMSPGIY 360
QY 361 SCLSGNTSACMYKTEGALTTPYMTLKGSVIANCKMTTCRCADPPGIIISQNGEAVSLID 420
Db 361 SCLSGNTSACMYKTEGALTTPYMTLKGSVIANCKMTTCRCADPPGIIISQNGEAVSLID 420
QY 421 RQSCNVLSLDGHTLRLSGEFDATYQKNISIODSQVIVTGNLIDISTELGNVNNISNALDK 480
Db 421 RQSCNVLSLDGHTLRLSGEFDATYQKNISIODSQVIVTGNLIDISTELGNVNNISNALDK 480
QY 481 LEENSKLDKVNKLTSTLSALITYIVLTVISLVCGLSLVACVIMYKQKQOQKTLMLWG 540
Db 481 LEENSKLDKVNKLTSTLSALITYIVLTVISLVCGLSLVACVIMYKQKQOQKTLMLWG 540
QY 541 NNTLDQMRATT 551
Db 541 NNTLDQMRATT 551
```

RESULT 6

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Q80KT13 ID Q80T13 PRELIMINARY; PRT; 551 AA.
AC Q80KT13;
DT 01-JUN-2002 (TremBLrel. 21, Created)
DT 01-JUN-2002 (TremBLrel. 21, Last sequence update)
DT 01-JUN-2003 (TremBLrel. 24, Last annotation update)
DE Fusion protein (Fragment).
OS Newcastle disease virus.
OC Viruses; ssRNA negative-strand viruses; Mononegavirales;
OC Paramyxoviridae; Paramyxovirinae; Rubulavirus.
OX NCBI_TaxID=11176;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=JS-1/97;
RA Ni X., Wu Y., Liu X.;
RT "Molecular epizootiological study of chicken Newcastle disease (ND) in east China.";
RL Zhongguo jiaqin 0:0-0(2002).
DR EMBL; AF458022; AAM13436.1; -
DR GO; GO:0019039; F:viral-cell fusion molecule activity; IEA.
DR GO; GO:0006948; P:viral-induced cell-cell fusion; IEA.
DR InterPro; IPR000776; Fusion_gly.
DR Pfam; PF00523; fusion_gly; 1.
FT NON TR 551
SQ SEQUENCE 551 AA; 58730 MW; 93CEE2D9E1947BFA CRC64;
```

```
Query Match 95.1%; Score 2621; DB 12; Length 551;
Best Local Similarity 95.1%; Pred. No. 4.4e-161;
Matches 524; Conservative 9; Mismatches 18; Indels 0; Gaps 0;
QY 1 MGRSSSTRIPVPLMLTVRVALALSCVPTSSLDGRPLAAAGIVVTGDKAVNIYSSQTGS 60
Db 1 MGRSSSTRIPVPLMLTVRVALALSCVPTSSLDGRPLAAAGIVVTGDKAVNIYSSQTGS 60
QY 61 IIVXLLPNPKDKEACAPLEAYNRTLTLLTPLGDSIRRIQESATTSGGRRQRFICA 120
```

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Db 61 IIVXLLPNPKDKEACAPLEAYNRTLTLLTPLGDSIRRIQESATTSGGRRQRFICA 120
QY 121 IIGGAALGVATAAQITTAASALIQAQNAANILRLKERIAATNEAVHEVTDGLSOLAVAG 180
Db 121 IIGSVLGVATAAQITTAASALIQAQNAANILRLKERIAATNEAVHEVTDGLSOLAVAG 180
QY 181 KMOQFVNDQFNKTAQELDCIKITQOVGVNELNYLTTELTTVFGPQITSPALTIQALYN 240
Db 181 KMOQFVNDQFNKTAQELDCIKITQOVGVNELNYLTTELTTVFGPQITSPALTIQALYN 240
QY 241 LAGNMDYLLTKLGVGNQSLIGSLITGNPIYDSOTQLLGIQVTLPSVGNLNNMRA 300
Db 241 LAGNMDYLLTKLGVGNQSLIGSLITGNPIYDSOTQLLGIQVTLPSVGNLNNMRA 300
QY 301 TYLETSLVSTTKGFASALVPKVMKGVSVBELDTSYCIETDLDLYCTRIVTFPMSPGIY 360
Db 301 TYLETSLVSTTKGFASALVPKVMKGVSVBELDTSYCIETDLDLYCTRIVTFPMSPGIY 360
QY 361 SCLSGNTSACMYKTEGALTTPYMTLKGSVIANCKMTTCRCADPPGIIISQNGEAVSLID 420
Db 361 SCLSGNTSACMYKTEGALTTPYMTLKGSVIANCKMTTCRCADPPGIIISQNGEAVSLID 420
QY 421 RQSCNVLSLDGHTLRLSGEFDATYQKNISIODSQVIVTGNLIDISTELGNVNNISNALDK 480
Db 421 RQSCNVLSLDGHTLRLSGEFDATYQKNISIODSQVIVTGNLIDISTELGNVNNISNALDK 480
QY 481 LEENSKLDKVNKLTSTLSALITYIVLTVISLVCGLSLVACVIMYKQKQOQKTLMLWG 540
Db 481 LEENSKLDKVNKLTSTLSALITYIVLTVISLVCGLSLVACVIMYKQKQOQKTLMLWG 540
QY 541 NNTLDQMRATT 551
Db 541 NNTLDQMRATT 551
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RESULT 7

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Q80KD0 ID Q80KD0 PRELIMINARY; PRT; 553 AA.
AC Q80KD0;
DT 01-JUN-2003 (TremBLrel. 24, Created)
DT 01-JUN-2003 (TremBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TremBLrel. 25, Last annotation update)
DE Fusion protein.
OS Newcastle disease virus.
OC Viruses; ssRNA negative-strand viruses; Mononegavirales;
OC Paramyxoviridae; Paramyxovirinae; Rubulavirus.
OX NCBI_TaxID=11176;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=HB92;
RA Pan Z.S., Chen Y.D., Shao H.B., Yang J., Xiong Z.L., Wen G.Y.,
RA Zhang C.Y.;
RT "Complete sequence for HB92 strain of Newcastle disease virus.";
RL Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=HB92;
RA Shao H.B., Yang J., Xiong Z.L.;
RL Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY225110; AAO46783.1; -
DR GO; GO:0019039; F:viral-cell fusion molecule activity; IEA.
DR GO; GO:0006948; P:viral-induced cell-cell fusion; IEA.
DR InterPro; IPR000776; Fusion_gly.
DR Pfam; PF00523; fusion_gly; 1.
SQ SEQUENCE 553 AA; 58886 MW; E336AEF87E9D655E CRC64;
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Query Match 95.1%; Score 2621; DB 12; Length 553;
Best Local Similarity 93.7%; Pred. No. 4.4e-161;
Matches 518; Conservative 20; Mismatches 15; Indels 0; Gaps 0;
QY 1 MGRSSSTRIPVPLMLTVRVALALSCVPTSSLDGRPLAAAGIVVTGDKAVNIYSSQTGS 60
Db 1 MGRSSSTRIPVPLMLTVRVALALSCVPTSSLDGRPLAAAGIVVTGDKAVNIYSSQTGS 60
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```
QY 61 IIVKLLPNMPKDEACAKAPLEAYNRTLTLLTPLGDSIRRIQESVTTSGGKQGRLLGA 120
Db 61 IIVKLLPNLPKDEACAKAPLDAYNRTLTLLTPLGDSIRRIQESVTTSGGKQGRLLGA 120
QY 121 IIGGAALGVATAAQITAAASALIQANQANAANILRLKERIAATNEAVEHVDGSLQAVAG 180
Db 121 IIGGVALGVATAAQITAAALIQAKNAANILRLKESIAATNEAVEHVDGSLQAVAG 180
QY 181 KMQQFVNDQFNKTAQELDCIKITQQVGVNELNLYLTTLTTFVFPQITSPALTIQALYN 240
Db 181 KMQQFVNDQFNKTAQELDCIKIAQQVGVNELNLYLTTLTTFVFPQITSPALNKLTIOALYN 240
QY 241 LAGGNDYLLTKLGVGNOLSSLIIGSLITGNPILYDSOTQLLGIQVTLPSVGNLNMRA 300
Db 241 LAGGNDYLLTKLGVGNOLSSLIIGSLITGNPILYDSOTQLLGIQVTLPSVGNLNMRA 300
QY 301 TYLETLSVSTTKGFASALVPKVMKGVSVIEELDTSYCIETDLDLYCTRIVTFPMSPGIY 360
Db 301 TYLETLSVSTTKGFASALVPKVTQVGVSVIEELDTSYCIETDLDLYCTRIVTFPMSPGIY 360
QY 361 SCLSGNTSACMSKTEGALTTPYMTLKGSVIANCKMTTCRCADPPGIIISQNYGEAVSLID 420
Db 361 SCLSGNTSACMSKTEGALTTPYMTIKGSVIANCKMTTCRCVNPPIISQNYGEAVSLID 420
QY 421 ROSCNVSLDGIITRLSGEFDATYQKNISIQDSQVITGNLDISTELGNVNNISNALDK 480
Db 421 KQSCNVSLGGITRLSGEFDTYQKNISIQDSQVITGNLDISTELGNVNNISNALNK 480
QY 481 LEESNKLDKVNKLTSTALITYIVLTISLVCGILSLVLACYLKYKQAKQKTLWLIG 540
Db 481 LEESNKLDKVNKLTSTALITYIVLTISLVFGILSLILACYLKYKQAKQKTLWLIG 540
QY 541 NNTLQDMRATTM 553
Db 541 NNTLQDMRATTM 553

RESULT 8
Q9NMH7 PRELIMINARY; PRT; 553 AA.
AC Q9NMH7;
DT 01-NOV-1999 (TrEMBLrel. 12, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Fusion protein.
GN F.
OS Newcastle disease virus.
OC Viruses; ssRNA negative-strand viruses; Mononegavirales;
OC Paramyxoviridae; Paramyxovirinae; Rubulavirinae; Rubulavirus.
OX NCBI_TaxID=11176;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20047980; PubMed=10580061;
RA Roemer-Oberdoerfer A., Mundt E., Mebatsion T., Buchholz U.J.,
RA Mettenleiter T.C.;
RT "Generation of recombinant lentogenic Newcastle Disease Virus from
RT cDNA.";
RL J. Gen. Virol. 80:2987-2995(1999).
RN [2]
RP SEQUENCE FROM N.A.
RA Roemer-Oberdoerfer A.;
RL Submitted (MAR-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; Y18898; CAB51325.1; -.
DR GO; GO:0019039; F:Viral-cell fusion molecule activity; IEA.
DR GO; GO:0006948; P:Viral-induced cell-cell fusion; IEA.
DR InterPro; IPR000776; Fusion gly.
DR Pfam; PF00523; fusion_gly; I.
SQ SEQUENCE 553 AA; 58868 MW; 1D2D10C09DC6E36B CRC64;

Query Match 95.0%; Score 2619; DB 12; Length 553;
Best Local Similarity 93.7%; Pred. No. 6e-161;
Matches 518; Conservative 19; Mismatches 16; Indels 0; Gaps 0;
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RESULT 9

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ID O90339 PRELIMINARY; PRT; 553 AA.
AC O90339;
DT 01-NOV-1998 (TrEMBLrel. 08, Created)
DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Fusion protein F.
GN F.
OS Newcastle disease virus.
OC Viruses; ssRNA negative-strand viruses; Mononegavirales;
OC Paramyxoviridae; Paramyxovirinae; Rubulavirinae; Rubulavirus.
OX NCBI_TaxID=11176;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99131394; PubMed=9934695;
RA de Leeuw O., Peeters B.;
RT "Complete nucleotide sequence of Newcastle disease virus: evidence for
RT the existence of a new genus within the subfamily Paramyxovirinae.";
RL J. Gen. Virol. 80:131-136(1999).
RN [2]
RP SEQUENCE FROM N.A.
RX STRAIN=LaSota;
RA de Leeuw O.S., Peeters B.P.H.;
RL Submitted (JUL-1998) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RX STRAIN=ZJ/2000;
RA Zhou J.Y., Ye J.X., Chen Q.X., Chen J.G., Cheng L.Q., Wang J.Y.;
RT "Newcastle disease virus Strain ZJ/2000.";
```

Submitted (AUG-2002) to the EMBL/GenBank/DBJ databases.
RL EMBL: AF077761; AAC28374.1; -
DR EMBL: AF534997; AAN01226.1; -
DR GO: 0019039; F: viral-cell fusion molecule activity; IEA.
DR GO: 0006948; P: viral-induced cell-cell fusion; IEA.
DR InterPro: IPR000776; Fusion_gly.
DR Pfam: PF00523; fusion_gly; 1.
SQ SEQUENCE 553 AA; 58896 MW; 4D29AEF87E4255B0 CRC64;

Query Match 94.9%; Score 2616; DB 12; Length 553;
Best Local Similarity 93.5%; Pred. No. 9.3e-161;
Matches 517; Conservative 20; Mismatches 16; Indels 0; Gaps 0;

QY 1 MGRSRSTRIPVPLMLTVRVALALSCVPTSLDGRPLAAAGIVVTGKAVNIYSSQTGS 60
DB 1 MGRSPSTKNPAPMMLTIRVALVLSICIPANSIDGRPLAAAGIVVTGKAVNIYSSQTGS 60
QY 61 IIVKLLNPMKDKKACAKAPLEAYNRTLTLLTPLGDSIRRIQESVTTSGGKQGRLLGA 120
DB 61 IIVKLLNPMKDKKACAKAPLEAYNRTLTLLTPLGDSIRRIQESVTTSGGKQGRLLGA 120
QY 121 IIGGAALGVATAAQITAAALIOANNAANILRLKERIAATNEAVHEVTDGLSOLAVAG 180
DB 121 IIGGAALGVATAAQITAAALIOANNAANILRLKERIAATNEAVHEVTDGLSOLAVAG 180
QY 181 KMQOFVNDQFNKTAQELDCIKITQOVGVNLMNLYLTTLTTFVGPQITSPALNTIQALYN 240
DB 181 KMQOFVNDQFNKTAQELDCIKITQOVGVNLMNLYLTTLTTFVGPQITSPALNTIQALYN 240
QY 241 LAGNMDYLLTKLGVGNQNLSSLGSLITGNPILYDSQTLLGIQVTLPSVGNLNNRA 300
DB 241 LAGNMDYLLTKLGVGNQNLSSLGSLITGNPILYDSQTLLGIQVTLPSVGNLNNRA 300
QY 301 TYLETLSVSTTKGFASALVPKVMKGVSVIEELDTSCIEETDLDYCTRIVTFPMSPGIY 360
DB 301 TYLETLSVSTTKGFASALVPKVMKGVSVIEELDTSCIEETDLDYCTRIVTFPMSPGIY 360
QY 361 SCLSGNTSACMSYKTEGALTTPYMTLKGSVIANCKMTTCRCADPPGIISQNYGEAVSLID 420
DB 361 SCLSGNTSACMSYKTEGALTTPYMTLKGSVIANCKMTTCRCADPPGIISQNYGEAVSLID 420
QY 421 RQSCNVLSLGGITLRLSGEFDATYQKNISIQDSQVITGNLDISTELGNVNNISNALDK 480
DB 421 RQSCNVLSLGGITLRLSGEFDATYQKNISIQDSQVITGNLDISTELGNVNNISNALDK 480
QY 481 LEESNRKLDKVNKLTSTALITVITVLSLGVLSLACVLMYKQAKQAQKTLWLIG 540
DB 481 LEESNRKLDKVNKLTSTALITVITVLSLGVLSLACVLMYKQAKQAQKTLWLIG 540
QY 541 NNTLDQMRATTKM 553
DB 541 NNTLDQMRATTKM 553

RESULT 10
Q91AH8 PRELIMINARY; PRT; 553 AA.
AC Q91AH8;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Fusion protein.
GN F.
OS Newcastle disease virus.
OC Viruses; ssRNA negative-strand viruses; Mononegavirales;
OC Paramyxoviridae; Paramyxovirinae; Rubulavirus.
OX NCBI_TaxID=11176;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=B1;
RX MEDLINE=21548317; PubMed=11689668;
RA Nakaya T., Cros J., Park M.S., Nakaya Y., Zheng H., Sagrera A.,
Villar E., Garcia-Sastre A., Palese P.

"Recombinant newcastle disease virus as a vaccine vector."; J. Virol. 75:11868-11873 (2001).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=B1;
RA Nakaya T., Garcia-Sastre A., Palese P.;
RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF375823; AAK55550.1; -
DR GO: 0019039; F: viral-cell fusion molecule activity; IEA.
DR GO: 0006948; P: viral-induced cell-cell fusion; IEA.
DR InterPro: IPR000776; Fusion_gly.
DR Pfam: PF00523; fusion_gly; 1.
SQ SEQUENCE 553 AA; 58910 MW; F09767CFDCE4493 CRC64;

Query Match 94.8%; Score 2615; DB 12; Length 553;
Best Local Similarity 93.3%; Pred. No. 1.1e-160;
Matches 516; Conservative 21; Mismatches 16; Indels 0; Gaps 0;

QY 1 MGRSRSTRIPVPLMLTVRVALALSCVPTSLDGRPLAAAGIVVTGKAVNIYSSQTGS 60
DB 1 MGRSPSTKNPAPMMLTIRVALVLSICIPANSIDGRPLAAAGIVVTGKAVNIYSSQTGS 60
QY 61 IIVKLLNPMKDKKACAKAPLEAYNRTLTLLTPLGDSIRRIQESVTTSGGKQGRLLGA 120
DB 61 IIVKLLNPMKDKKACAKAPLEAYNRTLTLLTPLGDSIRRIQESVTTSGGKQGRLLGA 120
QY 121 IIGGAALGVATAAQITAAALIOANNAANILRLKERIAATNEAVHEVTDGLSOLAVAG 180
DB 121 IIGGAALGVATAAQITAAALIOANNAANILRLKERIAATNEAVHEVTDGLSOLAVAG 180
QY 181 KMQOFVNDQFNKTAQELDCIKITQOVGVNLMNLYLTTLTTFVGPQITSPALNTIQALYN 240
DB 181 KMQOFVNDQFNKTAQELDCIKITQOVGVNLMNLYLTTLTTFVGPQITSPALNTIQALYN 240
QY 241 LAGNMDYLLTKLGVGNQNLSSLGSLITGNPILYDSQTLLGIQVTLPSVGNLNNRA 300
DB 241 LAGNMDYLLTKLGVGNQNLSSLGSLITGNPILYDSQTLLGIQVTLPSVGNLNNRA 300
QY 301 TYLETLSVSTTKGFASALVPKVMKGVSVIEELDTSCIEETDLDYCTRIVTFPMSPGIY 360
DB 301 TYLETLSVSTTKGFASALVPKVMKGVSVIEELDTSCIEETDLDYCTRIVTFPMSPGIY 360
QY 361 SCLSGNTSACMSYKTEGALTTPYMTLKGSVIANCKMTTCRCADPPGIISQNYGEAVSLID 420
DB 361 SCLSGNTSACMSYKTEGALTTPYMTLKGSVIANCKMTTCRCADPPGIISQNYGEAVSLID 420
QY 421 RQSCNVLSLGGITLRLSGEFDATYQKNISIQDSQVITGNLDISTELGNVNNISNALDK 480
DB 421 RQSCNVLSLGGITLRLSGEFDATYQKNISIQDSQVITGNLDISTELGNVNNISNALDK 480
QY 481 LEESNRKLDKVNKLTSTALITVITVLSLGVLSLACVLMYKQAKQAQKTLWLIG 540
DB 481 LEESNRKLDKVNKLTSTALITVITVLSLGVLSLACVLMYKQAKQAQKTLWLIG 540
QY 541 NNTLDQMRATTKM 553
DB 541 NNTLDQMRATTKM 553

RESULT 11
Q8QTI2 PRELIMINARY; PRT; 551 AA.
ID Q8QTI2
AC Q8QTI2;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Fusion protein (fragment).
OS Newcastle disease virus.
OC Viruses; ssRNA negative-strand viruses; Mononegavirales;
OC Paramyxoviridae; Paramyxovirinae; Rubulavirus.
OX NCBI_TaxID=11176;
RN [1]
RP SEQUENCE FROM N.A.

RC	STRAIN=Zhd-1/85;
RA	Ni X., Wu Y., Liu X.;
RT	"Molecular epizootiological study of chicken Newcastle disease (ND) in
RT	east China.";
RL	Zhongguo Jiadin 0:0-0(2002).
DR	EMBL; AF458023; AAM13437.1; "
DR	GO; GO:0019039; F:viral-cell fusion molecule activity; IEA.
DR	GO; GO:0006948; P:viral-induced cell-cell fusion; IEA.
DR	InterPro; IPR000776; Fusion_gly.
DR	Pfam; PF00523; fusion_gly; 1.
FT	NON TBR 551 551
SQ	SEQUENCE 551 AA; 58672 MW; 870A15D9E1947FA3 CRC64;
Query Match 94.7%; Score 2612; DB 12; Length 551;	
Best Local Similarity 94.7%; Pred No. 1.7e-160;	
Matches 522; Conservative 9; Mismatches 20; Indels 0; Gaps 0;	
Qy	1 MGRSSSTRIPVPLMLTVRVALALSCVPTSSLDRGPLAAAGIVVTGDKAVNIYTSQTGS 60
Dd	1 MGPKSSTNVAPLMLTARIALASCRTLNSLDGRPLAAAGIVVTGDKAVNIYTSQTGS 60
Qy	61 II VKLLPNMPKDEACAKAPLEAYNRITLTLLTPLGDSIRRIQBSVTTSGGKGRLIGA 120
Dd	61 II VKLLPNMPKDEACAKAPLEAYNRITLTLLTPLGDSIRRIQBSATTSGGRRRFIGA 120
Qy	121 IIGGAALGVATAAQITAASALIQAANAAILRKERIAATNEAVHEVTDGLSLAVAVG 180
Dd	121 IIGSVALGVATAAQITAASALIQAANAAILRLKESIAATNEAVHEVTDGLSLAVAVG 180
Qy	181 KMQQFVNDFNKTAEELDCIKITOOVGVELNYLTELTTVFPGPQITSPALTOLTIQALYN 240
Dd	181 KMQQFVNDFNKTAEELDCIKITOOVGVELNYLTELTTVFPGPQITSPALTOLTIQALYN 240
Qy	241 LAGNMDDYLTLKLGVGNQLSSLTGSGLTGNTPLYDSOTQLLGIQVTLPSVGNLNWRA 300
Dd	241 LAGNMDDYLTLKLGVGNQLSSLTGSGLTGNTPLYDSOTQLLGIQVTLPSVGNLNWRA 300
Qy	301 TYLETLSVSTTKGFASALVPKVVMKVSVEELDTSYCTIEDDLXYCTRIVTFPMSPGIY 360
Dd	301 TYLETLSVSTTKGFASALVPKVWTQVGSVEELDTSYCVETDDLXYCTRIVTFPMSPGIY 360
Qy	361 SCLSGNTSACWYSKTEGALTTPYMTLKXSVIANCKMTTCRCADPPGIIISQNYGEAVSLID 420
Dd	361 SCLSGNTSACWYSKTEGALTTPYMTLKXSVIANCKMTTCRCADPPGIIISQNYGEAVSLID 420
Qy	421 RQSQNLVLSDGITLRLSGEDPATYQKNISIQDSQVIITGNLDTSTELGNVNNNISNALDK 480
Dd	421 RHSQNLVLSDGITLRLSGEDPVTYQKNISILDSQVIITGNLDTSTELGNVNNNISNALDK 480
Qy	481 LEESNSKLDKVNKVLGTSTALITYIVLTVISLVCGILSLVLACYLMTKYQAQOKLLWLG 540
Dd	481 LEESNSKLDKVNKVLGTSTALITYIVLTVISLVCGILSLVLACYLMTKYQAQOKALLWLG 540
Qy	541 NNTLDQWRATT 551
Dd	541 NNTLDQWRATT 551

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RESULT 12
Q9WLE2
ID Q9WLE2
AC Q9WLE2; PRELIMINARY; PRT; 553 AA.
DT 01-NOV-1999 (TrEMBLrel. 12, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Fusion protein.
DE F.
GN F.
OS Newcastle disease virus.
OC Viruses; ssRNA negative-strand viruses; Mononegavirales;
OC Paramyxoviridae; Paramyxovirinae; Rubulavirus.
OX NCBI_TaxID=11176;
   {1}
RN
RP SEQUENCE FROM N.A.

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RC	STRAIN=DBS;
RA	Cao D.J., Yuan C.X., Guo X., Min P., Kong X.G., Lu J.L.;
RT	"Genetic Variance Analysis of F Gene of NDV From China.";
RL	Submitted (JUL-1998) to the EMBL/GenBank/DDBJ databases.
DR	EMBL; AF079323; AAC62244.1;
DR	GO; GO:0019039; F:viral-cell fusion molecule activity; IEA.
DR	GO; GO:0006948; P:viral-induced cell-cell fusion; IEA.
DR	InterPro; IPR000776; Fusion gly.
DR	Pfam; PF00523; fusion gly; 1.
SQ	SEQUENCE 553 AA; 58312 MW; 513469F7DBB805B4 CRC64;

Query Match	94.7%; Score 2611; DB 12; Length 553;
Best Local Similarity	93.3%; Pred.No.2e-160;
Matches 516; Conservative 20; Mismatches 17; Indels 0; Gaps 0;	

Qy	1	MGSRSSTRIPVLMLTVRVALALSCVCPTSSLDGRPLAAAGIVVTGDKAVNIYTSQTGS	60
Dd	1	MGSRPSTKNPAPMLLTIRVALVLSICIFANSIDGRPLAAAGI VVTGDKAVNIYTSQTGS	60
		: : : : :	
Qy	61	IIVKLLPNMKDEACAKAPLEAYNRITLTLLPLGDSIRRIQBSVTTSGGGKQGRLLGA	120
Dd	61	IIVKLLPNLPKDEACAKAPLDAYNRITLTLLPLGDSIRRIQBSVTTSGGGKQGRLLGA	120
		: : : : :	
Qy	121	IIGGAALGVATAQAQITTAASALI QANNAAILRLKERIAATNEAVHEVTDGLSQLAVVG	180
Dd	121	IIGGVALGVATAQAQITAAAAAIQAKQNAAILRKESIAATNEAVHEVTDGLSQLAVVG	180
		: : : : :	
Qy	181	KMQQFVNDFNKTAQLDLCIKITQQCVELNLYLTTLTVFGQITSPALTQTILQALYN	240
Dd	181	KMQQFVNDFNKTAQLDLCIKIAQQGVLENLYLTTLTVFGQITSPALKTKILQALYN	240
		: : : : :	
Qy	241	LAGNM DYLLTKLGVGNNQLSSLIGSLITGNPIYDSOTQLLAGIQVTLPVSGNLNMRA	300
Dd	241	LAGNM DYLLTKLGVGNNQLSSLIGCLITGNPIYDSOTQLLAGIQVTLPVSGNLNMRA	300
		: : : : :	
Qy	301	TYLETLVSVTTKGFSALVPKVVMKGVSVIEELDTSYCIETDLDLXCTRIVTFPMSPGIY	360
Dd	301	TYLETLVSVTTGRFSALVPKVVTQVGVSVIEELDTSYCIETDLDLXCTRIVTFPMSPGIY	360
		: : : : :	
Qy	361	SLCSGNTSA CMYSKTEGALTTPWTLKGSVIANKMTTCRCADPGIIISONYGEAVSLID	420
Dd	361	SLCSGNTSA CMYSKTEGALTTPYTIKGSVIANKMTTCRCVNPFGIIISONYGEAVSLID	420
		: : : : :	
Qy	421	RQSCNVLSLGGITLRLSGFEDATYQKNISITQDSQVITVGNLIDISTELGNWNNSISNALDK	480
Dd	421	RQSCNVLSLGGITLRLSGFEDVTYQKNISITQDSQVITVGNLIDISTELGNWNNSISNALNK	480
		: : : : :	
Qy	481	LEESNRKL DKVNKLTSTSA LIYIVLTVISLVCGILSLVACYLMYKQKAQKTLLWL G	540
Dd	481	LEESNRKL DKVNKLTSTSA LIYIVLTISLVFGILSLVACYLMYKQKAQKTLLWL G	540
		: : : : :	
Qy	541	NNILDQMRATTKM 553	
Dd	541	NNILDQMRATTKM 553	
		: : : : :	

[illegible]

RT "Genetic Variance Analysis of F Gene of NDV From China.,"
RL Submitted (JUL-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF079324; AAC62245.1; -;
DR GO; GO:0019039; F:viral-cell fusion molecule activity; IEA.
DR GO; GO:0006948; P:viral-induced cell-cell fusion; IEA.
DR InterPro; IPR000776; Fusion gly.
DR Pfam; PF00523; fusion gly; I.
SQ SEQUENCE 553 AA; 58969 MW; 6C181D049F971302 CRC64;

Query Match 94.5%; Score 2606; DB 12; Length 553;
Best Local Similarity 93.1%; Pred. No. 4.1e-160;
Matches 515; Conservative 20; Mismatches 18; Indels 0; Gaps 0;

```
Qy 1 MGRSSSTRIPVPLMLTVRVALALSCVPTSLDGRPLAAAGIVVTGDKAVNIYSSQTGS 60
Db 1 MGRSPSTKNPVPMMLTVRVALVLSICIPANSIDGRPLAAAGIVVTGDKAVNIYSSQTGS 60
Qy 61 IIVKLLPNMPKDKEACAKAPLEAYNRTLTLLTPLDGSIIRIQESVTTSGGKGQRLIGA 120
Db 61 IIVKLLPNLPDKKEACAKAPLDAYNRTLTLLTPLDGSIIRIQESVTTSGGKGQRLIGA 120
Qy 121 IIGGALGVATAAQAITAASALIQANNAANILRLKERIAATNEAVEHVTGSLQAVAVG 180
Db 121 IIGGALGVATAAQAITAASALIQANNAANILRLKERIAATNEAVEHVTGSLQAVAVG 180
Qy 181 KMQOFVNDQFNKTAQELDCIKITQOVGVNELNLYLTTELTVFGPQITSPALTIQALYN 240
Db 181 KMQOFVNDQFNKTAQELDCIKIAQOVGVNELNLYLTTELTVFGPQITSPALTIQALYN 240
Qy 181 KMQOFVNDQFNKTAQELDCIKITQOVGVNELNLYLTTELTVFGPQITSPALTIQALYN 240
Db 181 KMQOFVNDQFNKTAQELDCIKIAQOVGVNELNLYLTTELTVFGPQITSPALTIQALYN 240
Qy 241 LAGNMDYLLTKLGVGNQSLIGSLITGNPILYDSQTQLLGIVQLTPSVGNLNNMRA 300
Db 241 LAGNMDYLLTKLGVGNQSLIGSLITGNPILYDSQTQLLGIVQLTPSVGNLNNMRA 300
Qy 301 TYLETSLVSTTKGFASALVPKVMKGVSVIEELDTSYCIETDLDLYCTRIVTFPMSPGIY 360
Db 301 TYLETSLVSTTKGFASALVPKVMKGVSVIEELDTSYCIETDLDLYCTRIVTFPMSPGIY 360
Qy 361 SCLSGNTSACMYKTEGALTTPYMTLKGSVIANCKMTTCRCADPPGIISQNYGEAVSLID 420
Db 361 SCLSGNTSACMYKTEGALTTPYMTLKGSVIANCKMTTCRCADPPGIISQNYGEAVSLID 420
Qy 421 ROSCNVSLDGTILRLSGEPDVTYQKNISIQDSQVITGNLIDISTELGNVNNISNALDK 480
Db 421 ROSCNVSLDGTILRLSGEPDVTYQKNISIQDSQVITGNLIDISTELGNVNNISNALDK 480
Qy 481 LEESNRKLDKVNKLTSTSAITYVLTIVSLVCGILSLVACVLMYKQKQAKTLLWLG 540
Db 481 LEESNRKLDKVNKLTSTSAITYVLTIVSLVCGILSLVACVLMYKQKQAKTLLWLG 540
Qy 541 NNTLDQMRATTKM 553
Db 541 NNTLDQMRATTKM 553
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RESULT 14

```
Q9WD11 PRELIMINARY; PRT; 553 AA.
ID Q9WD11
AC Q9WD11
DT 01-NOV-1999 (TrEMBLrel. 12, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DE Fusion protein.
OS Newcastle disease virus.
OC Viruses; ssRNA negative-strand viruses; Mononegavirales;
OC Paramyxoviridae; Paramyxovirinae; Rubulavirus.
OX NCBI_TaxID=11176;
RN [1]
RP SEQUENCE FROM N.A.
RA Sagrera A., Villar E.;
RL Submitted (OCT-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF099661; AAD28333.1; -;
DR GO; GO:0019039; F:viral-cell fusion molecule activity; IEA.
```

DR GO; GO:0006948; P:viral-induced cell-cell fusion; IEA.
DR InterPro; IPR000776; Fusion gly.
DR Pfam; PF00523; fusion gly; I.
SQ SEQUENCE 553 AA; 58890 MW; 4DF02A800E4531A4 CRC64;

Query Match 94.5%; Score 2605; DB 12; Length 553;
Best Local Similarity 93.1%; Pred. No. 4.8e-160;
Matches 515; Conservative 20; Mismatches 18; Indels 0; Gaps 0;

```
Qy 1 MGRSSSTRIPVPLMLTVRVALALSCVPTSLDGRPLAAAGIVVTGDKAVNIYSSQTGS 60
Db 1 MGRSPSTKNPVPMMLTVRVALVLSICIPANSIDGRPLAAAGIVVTGDKAVNIYSSQTGS 60
Qy 61 IIVKLLPNMPKDKEACAKAPLEAYNRTLTLLTPLDGSIIRIQESVTTSGGKGQRLIGA 120
Db 61 IIVKLLPNLPDKKEACAKAPLDAYNRTLTLLTPLDGSIIRIQESVTTSGGKGQRLIGA 120
Qy 121 IIGGALGVATAAQAITAASALIQANNAANILRLKERIAATNEAVEHVTGSLQAVAVG 180
Db 121 IIGGALGVATAAQAITAASALIQANNAANILRLKERIAATNEAVEHVTGSLQAVAVG 180
Qy 181 KMQOFVNDQFNKTAQELDCIKITQOVGVNELNLYLTTELTVFGPQITSPALTIQALYN 240
Db 181 KMQOFVNDQFNKTAQELDCIKIAQOVGVNELNLYLTTELTVFGPQITSPALTIQALYN 240
Qy 241 LAGNMDYLLTKLGVGNQSLIGSLITGNPILYDSQTQLLGIVQLTPSVGNLNNMRA 300
Db 241 LAGNMDYLLTKLGVGNQSLIGSLITGNPILYDSQTQLLGIVQLTPSVGNLNNMRA 300
Qy 301 TYLETSLVSTTKGFASALVPKVMKGVSVIEELDTSYCIETDLDLYCTRIVTFPMSPGIY 360
Db 301 TYLETSLVSTTKGFASALVPKVMKGVSVIEELDTSYCIETDLDLYCTRIVTFPMSPGIY 360
Qy 361 SCLSGNTSACMYKTEGALTTPYMTLKGSVIANCKMTTCRCADPPGIISQNYGEAVSLID 420
Db 361 SCLSGNTSACMYKTEGALTTPYMTLKGSVIANCKMTTCRCADPPGIISQNYGEAVSLID 420
Qy 421 ROSCNVSLDGTILRLSGEPDVTYQKNISIQDSQVITGNLIDISTELGNVNNISNALDK 480
Db 421 ROSCNVSLDGTILRLSGEPDVTYQKNISIQDSQVITGNLIDISTELGNVNNISNALDK 480
Qy 481 LEESNRKLDKVNKLTSTSAITYVLTIVSLVCGILSLVACVLMYKQKQAKTLLWLG 540
Db 481 LEESNRKLDKVNKLTSTSAITYVLTIVSLVCGILSLVACVLMYKQKQAKTLLWLG 540
Qy 541 NNTLDQMRATTKM 553
Db 541 NNTLDQMRATTKM 553
```

RESULT 15

```
Q91HX4 PRELIMINARY; PRT; 553 AA.
ID Q91HX4
AC Q91HX4;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DE Fusion protein.
OS Newcastle disease virus.
OC Viruses; ssRNA negative-strand viruses; Mononegavirales;
OC Paramyxoviridae; Paramyxovirinae; Rubulavirus.
OX NCBI_TaxID=11176;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=NDV-JL-1/97;
RA Ningyi J.;
RT "Variabilities Analysis of HN Protein Gene among the NDV Strain
RT Changli and Strains Offshore.,"
RL Chin. J. Vet. Sci. 20:328-331(2000).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=NDV-JL-1/97;
RA Ningyi J., Xinglong W., Zhuang D.;
```


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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: April 18, 2004, 01:19:18 ; Search time 46 Seconds
(without alignments)
1156.389 Million cell updates/sec

Title: US-10-725-841-2

Perfect score: 2757

Sequence: 1 MGSRSSTRIPVPLMLTVRVA.....KTLMLGNNTLDQMRATTKM 553

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR 78:*
1: pirl:*
2: pirl2:*
3: pirl3:*
4: pirl4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2724	98.8	553	1 VGNZU1	cell fusion glycop
2	2724	98.8	553	1 A46329	cell fusion glycop
3	2691	97.6	553	2 S23621	gene F protein - N
4	2684	97.4	553	1 B46329	cell fusion glycop
5	2658	96.4	553	2 S38785	gene F protein - N
6	2625	95.2	553	1 H46329	cell fusion glycop
7	2622	95.1	553	1 D46329	cell fusion glycop
8	2606	94.5	553	1 VGNZTE	cell fusion glycop
9	2603	94.4	553	1 VGNZNV	cell fusion glycop
10	2602	94.4	553	2 S40163	cell fusion glycop
11	2599	94.3	553	2 S06345	cell fusion protei
12	2598	94.2	553	1 A36830	cell fusion glycop
13	2593	94.1	553	1 G46329	cell fusion glycop
14	2592	94.0	553	1 B36830	cell fusion glycop
15	2589	93.9	553	1 VGNZGB	cell fusion glycop
16	2588	93.9	553	1 E46329	cell fusion glycop
17	2585	93.8	553	1 I46329	cell fusion glycop
18	2579	93.5	553	1 VGNZND	cell fusion glycop
19	2575	93.4	553	2 S38784	gene F protein - N
20	2555	92.7	553	2 S23622	gene F protein - N
21	2554	92.6	553	2 S23620	F protein - Newcas
22	2549	92.5	553	2 S38786	gene F protein - N
23	1018.5	36.9	534	2 A37483	F protein - Muraya
24	717	26.0	529	1 VGNZSP	cell fusion glycop
25	712.5	25.8	538	1 VGNZMW	cell fusion protei
26	712.5	25.8	538	2 S52472	cell fusion glycop
27	704	25.5	538	1 VGNZMS	cell fusion protei
28	704	25.5	551	1 VGNZP2	cell fusion glycop
29	701.5	25.4	538	1 VGNZMU	cell fusion glycop

ALIGNMENTS

RESULT 1

VGNZU1

cell fusion glycoprotein precursor - Newcastle disease virus (strains Ulster and ULS/67)

N;Contains: fusion glycoprotein F1; fusion glycoprotein F2

C;Species: Newcastle disease virus

C;Date: 30-Jun-1989 #sequence_revision 30-Jun-1989 #text_change 16-Jun-2000

C;Accession: A29823; C46329

R;Miller, N.S.; Chambers, P.; Emerson, P.T.

J. Gen. Virol. 69, 613-620, 1988

A;Title: Nucleotide sequence of the fusion and haemagglutinin-neuraminidase glycoprotein ns.

A;Reference number: A92799; MUID:88171450; PMID:3351479

A;Accession: A29823

A;Molecule type: mRNA

A;Residues: 1-553 <ML>

A;Cross-references: GB:D00243; NID:g222174; PIDN:BAA00173.1; PID:g222175

A;Experimental source: strain Ulster

R;Toyoda, T.; Sakaguchi, T.; Hirota, H.; Gotoh, B.; Kuma, K.; Miyata, T.; Nagai, Y.

Virology 169, 273-282, 1989

A;Title: Newcastle disease virus evolution. II. Lack of gene recombination in generating A;Reference number: A46329; MUID:89204898; PMID:2705298

A;Accession: C46329

A;Molecule type: Genomic RNA

A;Residues: 1-553 <TOY>

A;Cross-references: GB:M24694; NID:g293923; PIDN:AAA46645.1; PID:g293924

A;Experimental source: strain ULS/67

C;Genetics:

A;Gene: F

C;Superfamily: parainfluenza virus cell fusion protein

C;Keywords: glycoprotein; membrane fusion; transmembrane protein

F;1-25/Domain: signal sequence #status predicted <SIG>

F;26-117/Product: cell fusion glycoprotein F2 #status predicted <PF2>

F;118-553/Product: cell fusion glycoprotein F1 #status predicted <PF1>

F;495-528/Domain: transmembrane #status predicted <TMN>

F;85,191,366,447,471/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match

Best Local Similarity 98.8%; Score 2724; DB 1; Length 553;

Matches 548; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 MGSRSSTRIPVPLMLTVRVALSCVPTSSLDGRLAAGIIVTGDKAVNIYTSQTGS 60

Db 1 MGSRSSTRIPVPLMLTVRVALSCVPTSSLDGRLAAGIIVTGDKAVNIYTSQTGS 60

QY 61 IIVKLLPNPKDKEACAPLEAYNRTLTLLTPLGDSIRRIQESVTTSGGKQRLIGA 120

Db 61 IIVKLLPNPKDKEACAPLEAYNRTLTLLTPLGDSIRRIQESVTTSGGKQRLIGA 120

QY 121 IIGGAALGVATAAQITAAASALITQANNAANILRLKERTAAATNEAVHEVTDGLSQAIVG 180

Db 121 IIGGAALGVATAAQITAAASALITQANNAANILRLKERTAAATNEAVHEVTDGLSQAIVG 180

Qy	181	KMOQFVNDQFNKTAQELDCIKITQOQGVNELNLYLTETLTVFGPQITSPALTQLTITQALYN	240
Db	181	KMOQFVNDQFNKTAQELDCIKITQOQGVNELNLYLTETLTVFGPQITSPALTQLTITQALYN	240
Qy	241	LAGNMDYLLTKLGVGNQNLSSLIGSLITGNPILYDSOTQLIGIQVTLPSVGNLNNMRA	300
Db	241	LAGNMDYLLTKLGVGNQNLSSLIGSLITGNPILYDSOTQLIGIQVTLPSVGNLNNMRA	300
Qy	301	TYLETLSVSTTKGFASALVPKVMKGVSVIEBELDTSYCIETDLDLYCTRIVTFPMSPGIY	360
Db	301	TYLETLSVSTTKGFASALVPKVMQVGVSVIEBELDTSYCIETDLDLYCTRIVTFPMSPGIY	360
Qy	361	SCLSGNTSACMYSKTEGALTTPYMYTLKGSVIANCKMTTCRCADPPGIIISQNYGEAVSLID	420
Db	361	SCLSGNTSACMYSKTEGALTTPYMYTLKGSVIANCKMTTCRSADPPGIIISQNYGEAVSLID	420
Qy	421	ROSCNVLSLDGTTILRLSGEFDATYQKNISIQDSQVIVTGNLIDISTELGNVNNISINALDK	480
Db	421	ROSCNVLSLDGTTILRLSGEFDATYQKNISIQDSQVIVTGNLIDISTELGNVNNISINALDK	480
Qy	481	LEENSCLDKVNVKLTSTTSALITYITVLTVISLVCGILSILVACYLWYKQAKQOKTLLMLG	540
Db	481	LEENSCLDKVNVKLTSTTSALITYITVLTVISLVCGILSILVACYLWYKQAKQOKTLLMLG	540
Qy	541	NTNLDQMRATTQK 553	
Db	541	NTNLDQMRATTQK 553	

RESULT 2

A46329
 cell fusion glycoprotein precursor - Newcastle disease virus (strain D26/76)
 N1:Contusions: fusion glycoprotein F1; fusion glycoprotein F2
 C:Species: Newcastle disease virus
 C:Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 16-Jul-1999
 C:Accession: A46329
 R:Toyoda, T.; Sakauchi, T.; Hirota, H.; Gotoh, B.; Kuma, K.; Miyata, T.; Nagai, Y.
 V:J. Virol. 169, 273-282, 1989
 A:Title: Newcastle disease virus evolution. II. Lack of gene recombination in general
 A:Reference number: A46329; MUID:89204898; PMID:2705298
 A:Accession: A46329
 A:Molecule type: Genomic RNA
 A:Residues: 1-553 <TOY>
 A:Cross-references: GB:M24692; NID:G293919; PIDN:AAA46643.1; PID:G293920
 C:Genetics:
 A:Gene: F
 C:Superfamily: parainfluenza virus cell fusion protein
 C:Keywords: Glycoprotein; membrane fusion; transmembrane protein
 F:1-25/Domain: signal sequence #status predicted <SIG>
 F:36-117/Product: cell fusion glycoprotein F2 #status predicted <FF2>
 F:118-553/Product: cell fusion glycoprotein F1 #status predicted <FF1>
 F:495-528/Domain: transmembrane #status predicted <TMN>
 F:85-191.366.447.471/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match	98.8%; Score 2724; DB 1; Length 553;
Best Local Similarity	98.4%; Pred. No. 1.4e-162;
Matches 544; Conservative	4; Mismatches 5; Indels 0; Gaps 0;
QY	1 MGRSSRTRIPVPLMLTVRVALALSCVPTSSLDGRPLAAAGIVTGDKAVNIYTSQTGS 60
DB	1 MGRSSRTRIPVPLMLTVRVALALSCVPTSSLDGRPLAAAGIVTGDKAVNIYTSQTGS 60
QY	61 IIVKLENNPKDKKACAKAPLEAYNRTLTTLLTPLGDSIRRIQBSVTTSGGKGRLTGA 120
DB	61 IIVKLENNPKDKKACAKAPLEAYNRTLTTLLTPLGDSIRRIQBSVTTSGGKGRLTGA 120
QY	121 IIGGAAIGVATAAGITTAASALIQAQNAANAIIIRLKERIAATNEAVEHTDGIQLAVAVG 180
DB	121 IIGGVALGVATAAGITTAASALIQAQNAANAIIIRLKESTAAATNEAVEHTDGLSQAQAVG 180
QY	181 KMQQFVNDQFNKTAQELDCIKITQQGVGVELNLYLTETVTFGPQITSPALQTITQALYN 240
DB	181 KMQQFVNDQFNKTAQELDCIKITQQGVGVELNLYLTETVTFGPQITSPALQTITQALYN 240

Qy	241	LAGNMDYLLTKLGVGNNOSSLIGSGLLITGNPTLYDSOTOLLGHQVTLTPSVGNLNNMRA	300
Db	241	LAGNMDYLLTKLGVGNNOSSLIGSGLLITGNPTLYDSOTOLLGHQVTLTPSVGNLNNMRA	300
Qy	301	TYLETLSVSTTKGFASALVPKVMKGVSVIBELDTSYCIETDLDLYCTRIVTFPMSPGIY	360
Db	301	TYLETLSVSTTKGFASALVPKVVTVQGVSVIBELDTSYCIETDLDLYCTRIVTFPMSPGIY	360
Qy	361	SCLSGNTSACMYSKTEGALTTPYMLTKGSVIANCKMTTCRCADPPGIIISQNYGEAVSLID	420
Db	361	SCLSGNTSACMYSKTEGALTTPYMLTKGSVIANCKMTTCRCADPPGIIISQNYGEAVSLID	420
Qy	421	RQSCNVILSDGITLURLSGEFPATYQKNISIQDSQVIVTGNLIDISTELGNVNNSISNALDK	480
Db	421	RQSCNVILSDGITLURLSGEFPATYQKNISIQDSQVIVTGNLIDISTELGNVNNSISNALDK	480
Qy	481	LEENSCLDKVNVKLTSLSALITVLTIVLSVCGILSLVLACYLMYKQAKQKTLWLIG	540
Db	481	LEENSCLDKVNVKLTSLSALITVLTIVLSVCGILSLVLACYLMYKQAKQKTLWLIG	540
Qy	541	NTTLDQMRATTYKM	553
Db	541	NTTLDQMRATTYKM	553

RESULT 3

S23621
gene F protein - Newcastle disease virus
C,Species: Newcastle disease virus
C,Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 25-Oct-1996
C,Accession: S23621
R:Pritzer, E.; Kuroda, K.; Garten, W.; Nagai, Y.; Klenk, H.D.
Virus Res. 15, 237-242, 1990
A,Title: A host range mutant of Newcastle disease virus with an altered cleavage site
A,Reference number: S23620; PMID:2188464
A,Accession: S23621
A,Status: preliminary
A,Molecule type: mRNA
A,Residues: 1-553 <PRI>
A,Cross-references: EMBL:Z12110
C,Superfamily: parainfluenza virus cell fusion protein

Query Match 97.6%; Score 2691; DB 2; Length 553;
Best Local Similarity 98.2%; Pred. No. 1.78-160;
Matches 543; Conservative 1; Mismatches 9; Indels 0; Gaps

Db 361 SCLSGNTSACWYKTEGALTTPYMTLKGSVIANCKMTTCRCADPPGIISQNYGEAVSLID 420
QY 421 RQSCNVSLDGIITRLSGEFDATYQKNISIQDSQVIVTGNLDISTELGNVNNISNALDK 480
Db 421 RQSCNVSLDGIITRLSGEFDATYQKNISIQDSQVIVTGNLDISTELGNVNNISNALDK 480
QY 481 LEESNSKLDKVNKLTSTALITYIVLTIVLSVCGILSLVACVLMYKQAKOQKTLMLWG 540
Db 481 LEESNSKLDKVNKLTSTALITYIVLTIVLSVCGILSLVACVLMYKQAKOQKTLMLWG 540
QY 541 NNTLDQMRATTM 553
Db 541 NNTLDQMRATTM 553

RESULT 4
B46329
cell fusion glycoprotein precursor - Newcastle disease virus (strain Que/66)
N/Contains: fusion glycoprotein F1; fusion glycoprotein F2
C/Species: Newcastle disease virus
C/Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 16-Jul-1999
C/Accession: B46329
R/Toyoda, T.; Sakaguchi, T.; Hirota, H.; Gotoh, B.; Kuma, K.; Miyata, T.; Nagai, Y.
Virology 169, 273-282, 1989
A/Title: Newcastle disease virus evolution. II. Lack of gene recombination in generating
A/Reference number: A46329; MUID:89204898; PMID:2705298
A/Accession: B46329
A/Molecule type: genomic RNA
A/Residues: 1-553 <TOY>
A/Cross-references: GB:M24693; NID:G293921; PIDN:AAA4644.1; PID:G293922
C/Genetics:
A/Gene: F
C/Superfamily: parainfluenza virus cell fusion protein
C/Keywords: glycoprotein; membrane fusion; transmembrane protein
F1-25/Domain: signal sequence #status predicted <SIG>
F26-117/Product: cell fusion glycoprotein F2 #status predicted <PF2>
F118-553/Product: cell fusion glycoprotein F1 #status predicted <PF1>
F495-528/Domain: transmembrane #status predicted <TMN>
F:85,191,366,447,471/Binding site: carbohydrate (Asn) #status predicted

Query Match 97.4%; Score 2684; DB 1; Length 553;
Best Local Similarity 97.3%; Pred. No. 4.5e-160;
Matches 538; Conservative 7; Mismatches 8; Indels 0; Gaps 0;

QY 1 MGSRSSTPIPVMLTVRVALALSCVPTSSLDGRPLAAGIVTGDKAVNIYTSQTGS 60
Db 1 MGSRSSTPIPVMLTVRVALALSCVPTSSLDGRPLAAGIVTGDKAVNIYTSQTGS 60
QY 61 IIVKLLPNPKDKEACAKAPLEAYNRTLTLTLPGLDSIRRIQESVTTSGGKQGRLLGA 120
Db 61 IIVKLLPNPKDKEACAKAPLEAYNRTLTLTLPGLDSIRRIQESVTTSGGKQGRLLGA 120
QY 121 IIGGVALGATAAQTAAAGIQAONAAIILRLKERIAATNEAVEHVTDGLSOLAVAVG 180
Db 121 IIGGVALGATAAQTAAAGIQAONAAIILRLKERIAATNEAVEHVTDGLSOLAVAVG 180
QY 181 KMQQFVNDQFNKTAQELDCIKITQQVGVNELNYLTETLTVFGPQITSPALTOITQALYN 240
Db 181 KMQQFVNDQFNKTAQELDCIKITQQVGVNELNYLTETLTVFGPQITSPALTOITQALYN 240
QY 241 LAGGNMDYLLTKLGVGNQLSSLSGLITGNPILYDSOTQLLGIQVTLPSVGNLNNMRA 300
Db 241 LAGGNMDYLLTKLGVGNQLSSLSGLITGNPILYDSOTQLLGIQVTLPSVGNLNNMRA 300
QY 301 TYLETLSVTTKGFASALVPKVMKGVSVIEELDTSYCIETDLCTRIYVTFPMSPGIY 360
Db 301 TYLETLSVTTKGFASALVPKVMKGVSVIEELDTSYCIETDLCTRIYVTFPMSPGIY 360
QY 361 SCLSGNTSACWYKTEGALTTPYMTLKGSVIANCKMTTCRCADPPGIISQNYGEAVSLID 420
Db 361 SCLSGNTSACWYKTEGALTTPYMTLKGSVIANCKMTTCRCADPPGIISQNYGEAVSLID 420
QY 421 RQSCNVSLDGIITRLSGEFDATYQKNISIQDSQVIVTGNLDISTELGNVNNISNALDK 480
Db 421 RQSCNVSLDGIITRLSGEFDATYQKNISIQDSQVIVTGNLDISTELGNVNNISNALDK 480
QY 481 LEESNSKLDKVNKLTSTALITYIVLTIVLSVCGILSLVACVLMYKQAKOQKTLMLWG 540
Db 481 LEESNSKLDKVNKLTSTALITYIVLTIVLSVCGILSLVACVLMYKQAKOQKTLMLWG 540
QY 541 NNTLDQMRATTM 553
Db 541 NNTLDQMRATTM 553

Db 421 RQSCNVSLDGIITRLSGEFDATYQKNISIQDSQVIVTGNLDISTELGNVNNISNALDK 480
QY 481 LEESNSKLDKVNKLTSTALITYIVLTIVLSVCGILSLVACVLMYKQAKOQKTLMLWG 540
Db 481 LEESNSKLDKVNKLTSTALITYIVLTIVLSVCGILSLVACVLMYKQAKOQKTLMLWG 540
QY 541 NNTLDQMRATTM 553
Db 541 NNTLDQMRATTM 553

RESULT 5
S38785
gene F protein - Newcastle disease virus
C/Species: Newcastle disease virus
C/Date: 06-Feb-1995 #sequence_revision 06-Feb-1995 #text_change 20-Sep-1999
C/Accession: S38785
R/Garten, W.D.
submitted to the EMBL Data Library, May 1992
A/Reference number: S22083
A/Accession: S38785
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-553 <GAR>
A/Cross-references: EMBL:Z121110; NID:G60658; PIDN:CAA78095.1; PID:G60659
C/Superfamily: parainfluenza virus cell fusion protein

Query Match 96.4%; Score 2658; DB 2; Length 553;
Best Local Similarity 96.9%; Pred. No. 1.9e-158;
Matches 536; Conservative 2; Mismatches 15; Indels 0; Gaps 0;

QY 1 MGSRSSTPIPVMLTVRVALALSCVPTSSLDGRPLAAGIVTGDKAVNIYTSQTGS 60
Db 1 MGSRSSTPIPVMLTVRVALALSCVPTSSLDGRPLAAGIVTGDKAVNIYTSQTGS 60
QY 61 IIVKLLPNPKDKEACAKAPLEAYNRTLTLTLPGLDSIRRIQESVTTSGGKQGRLLGA 120
Db 61 IIVKLLPNPKDKEACAKAPLEAYNRTLTLTLPGLDSIRRIQESVTTSGGKQGRLLGA 120
QY 121 IIGGVALGATAAQTAAAGIQAONAAIILRLKERIAATNEAVEHVTDGLSOLAVAVG 180
Db 121 IIGGVALGATAAQTAAAGIQAONAAIILRLKERIAATNEAVEHVTDGLSOLAVAVG 180
QY 181 KMQQFVNDQFNKTAQELDCIKITQQVGVNELNYLTETLTVFGPQITSPALTOITQALYN 240
Db 181 KMQQFVNDQFNKTAQELDCIKITQQVGVNELNYLTETLTVFGPQITSPALTOITQALYN 240
QY 241 LAGGNMDYLLTKLGVGNQLSSLSGLITGNPILYDSOTQLLGIQVTLPSVGNLNNMRA 300
Db 241 LAGGNMDYLLTKLGVGNQLSSLSGLITGNPILYDSOTQLLGIQVTLPSVGNLNNMRA 300
QY 301 TYLETLSVTTKGFASALVPKVMKGVSVIEELDTSYCIETDLCTRIYVTFPMSPGIY 360
Db 301 TYLETLSVTTKGFASALVPKVMKGVSVIEELDTSYCIETDLCTRIYVTFPMSPGIY 360
QY 361 SCLSGNTSACWYKTEGALTTPYMTLKGSVIANCKMTTCRCADPPGIISQNYGEAVSLID 420
Db 361 SCLSGNTSACWYKTEGALTTPYMTLKGSVIANCKMTTCRCADPPGIISQNYGEAVSLID 420
QY 421 RQSCNVSLDGIITRLSGEFDATYQKNISIQDSQVIVTGNLDISTELGNVNNISNALDK 480
Db 421 RQSCNVSLDGIITRLSGEFDATYQKNISIQDSQVIVTGNLDISTELGNVNNISNALDK 480
QY 481 LEESNSKLDKVNKLTSTALITYIVLTIVLSVCGILSLVACVLMYKQAKOQKTLMLWG 540
Db 481 LEESNSKLDKVNKLTSTALITYIVLTIVLSVCGILSLVACVLMYKQAKOQKTLMLWG 540
QY 541 NNTLDQMRATTM 553
Db 541 NNTLDQMRATTM 553

RESULT 6

H46329
cell fusion glycoprotein precursor - Newcastle disease virus
N:Contains: fusion glycoprotein F1; fusion glycoprotein F2
C:Species: Newcastle disease virus
C:Date: 31-Dec-1993 #sequence_revision 22-Oct-1999 #text_change 22-Oct-1999
C:Accession: S07422; H46329
R:McGuinness, L.W.; Morrison, T.G.
Virus Res. 5, 343-356, 1986
A:Title: Nucleotide sequence of the gene encoding the Newcastle disease virus fusion protein
A:Reference number: S07422; MUID:87044526; PMID:3776349
A:Accession: S07422
A:Molecule type: mRNA
A:Residues: 1-553 <MCG>
A:Cross-references: EMBL:M21881
A:Experimental source: Strain Australia-Victoria
R:Toyoda, T.; Sakaguchi, T.; Hirota, H.; Gotoh, B.; Kuma, K.; Miyata, T.; Nagai, Y.
Virology 169, 273-282, 1989
A:Title: Newcastle disease virus evolution. II. Lack of gene recombination in generating
A:Reference number: A46329; MUID:89204898; PMID:2705298
A:Accession: H46329
A:Molecule type: Genomic RNA
A:Residues: 1-65, 'H', 67-553 <TOY>
A:Cross-references: GB:M24700; NID:G293933; PIDN:AAA46650.1; PID:G293934
A:Experimental source: Strain AUS/32
C:Genetics:
A:Gene: F
C:Superfamily: parainfluenza virus cell fusion protein
C:Keywords: glycoprotein; membrane fusion; transmembrane protein
F:1-25/Domain: signal sequence #status predicted <SIG>
F:125-116/Product: cell fusion glycoprotein F2 #status predicted <FF2>
F:112-116/Region: cleavage processing #status predicted
F:117-553/Product: cell fusion glycoprotein F1 #status experimental <FF1>
F:499-526/Domain: transmembrane #status predicted <TM>
F:85,191,366,447,471/Binding site: carbohydrate (Asn) (covalent) #status predicted
F:85,191,366,447,471,541/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 95.2%; Score 2625; DB 1; Length 553;
Best Local Similarity 95.5%; Pred. No. 2.2e-156;
Matches 528; Conservative 6; Mismatches 19; Indels 0; Gaps 0;

Qy	1	MGRSSSTRIPVPLMLTVRVALSCVPTSSLDGRPLAAAGIVTGDKAVNIYSSQTGS	60
Db	1	MGRSSSTRIPVPLMLTVRVALSCVHLASSLDGRPLAAAGIVTGDKAVNIYSSQTGS	60
Qy	61	IIVKLLPNMPKDEACAKAPLEAYNRTLTLLTPLGDSIRRIQESVTTSGGKQRLIGA	120
Db	61	IIVKLLPNMPKDEACAKAPLEAYNRTLTLLTPLGDSIRRIQESVTTSGGRRQRFIGA	120
Qy	121	IIGGALGVATAAQITAAALIQANQANAILRLKERTAAATNEAVHEVTDGLSOLAVAVG	180
Db	121	IIGGALGVATAAQITAAALIQANQANAILRLKERTATATNEAVHEVTDGLSOLAVAVG	180
Qy	181	KMQQFVNDQFNKTAQELDCIKITQGVVELNLYLTETLTVFGPQITSPALQTTLTQALYN	240
Db	181	KMQQFVNDQFNNTAQELDCIKITQGVVELNLYLTETLTVFGPQITSPALQTTLTQALYN	240
Qy	241	LAGGNMVDLLTKLGVNNQLSSLGSLITGNPILYDSQTQLLGIQVTLPSVGNLNNMRA	300
Db	241	LAGGNMVDLLTKLGVNNQLSSLGSLITGNPILYDSQTQLLGIQVTLPSVGNLNNMRA	300
Qy	301	TYLETLSVSTTKGFASALVPKVMKGVSVIEBELDTSYCIETDLDYCTRTVTFPMSPGIY	360
Db	301	TYLETLSVSTTKGFASALVPKVVTVQGVSVIEBELDTSYCIETDLDYCTRTVTFPMSPGIY	360
Qy	361	SCLSGNTSACMSYKTEGALTTPYMTLKGSVIANCKMTTCRCADPPGIIISQNYGEAVSLID	420
Db	361	SCLNGNTSACMSYKTEGALTTPYMTLKGSVIANCKMTTCRCADPPGIIISQNYGEAVSLID	420
Qy	421	RQSCNVLSLDGTTLRLSGEFDATYQKNISIQDSQVIVTGNLDISTELGNVNNISNALDK	480
Db	421	RHSCNVLSLDGTTLRLSGEFDATYQKNISILDSQVIVTGNLDISTELGNVNNISNALDK	480

Qy	481	LEESNKLDKVNVKLTSTTSALITYIVLTIVTSVCGILSLVACLYMYKQAKQKTLWLIG	540
Db	481	LEESNKLDKVNVKLTSTTSALITYIATLSVCGILSLVACLYMYKQAKQKTLWLIG	540
Qy	541	NNTLDMQMRATTKM	553
Db	541	NNTLGQMRATTKM	553

RESULT 7

D46329
cell fusion glycoprotein precursor - Newcastle disease virus (strain BI/47)
N:Contains: fusion glycoprotein F1; fusion glycoprotein F2
C:Species: Newcastle disease virus
C:Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 16-Jul-1999
C:Accession: D46329
R:Toyoda, T.; Sakaguchi, T.; Hirota, H.; Gotoh, B.; Kuma, K.; Miyata, T.; Nagai, Y.
Virology 169, 273-282, 1989
A:Title: Newcastle disease virus evolution. II. Lack of gene recombination in generating
A:Reference number: A46329; MUID:89204898; PMID:2705298
A:Accession: D46329
A:Molecule type: Genomic RNA
A:Residues: 1-553 <TOY>
A:Cross-references: GB:M24695; NID:G293925; PIDN:AAA46646.1; PID:G293926
C:Genetics:
A:Gene: F
C:Superfamily: parainfluenza virus cell fusion protein
C:Keywords: glycoprotein; membrane fusion; transmembrane protein
F:1-25/Domain: signal sequence #status predicted <SIG>
F:26-117/Product: cell fusion glycoprotein F2 #status predicted <FF2>
F:118-553/Product: cell fusion glycoprotein F1 #status predicted <FF1>
F:495-528/Domain: transmembrane #status predicted <TM>
F:85,191,366,447,471/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 95.1%; Score 2622; DB 1; Length 553;
Best Local Similarity 93.5%; Pred. No. 3.4e-156;
Matches 517; Conservative 21; Mismatches 15; Indels 0; Gaps 0;

Qy	1	MGRSSSTRIPVPLMLTVRVALSCVPTSSLDGRPLAAAGIVTGDKAVNIYSSQTGS	60
Db	1	MGRSPSTKIPAPMMLTRIVLVLSICIPANSIDGRPLAAAGIVTGDKAVNIYSSQTGS	60
Qy	61	IIVKLLPNMPKDEACAKAPLEAYNRTLTLLTPLGDSIRRIQESVTTSGGKQRLIGA	120
Db	61	IIVKLLPNMPKDEACAKAPLDAYNRTLTLLTPLGDSIRRIQESVTTSGGRRQRLIGA	120
Qy	121	IIGGALGVATAAQITAAALIQANQANAILRLKERTAAATNEAVHEVTDGLSOLAVAVG	180
Db	121	IIGGALGVATAAQITAAALIQANQANAILRLKESITAAATNEAVHEVTDGLSOLAVAVG	180
Qy	181	KMQQFVNDQFNKTAQELDCIKITQGVVELNLYLTETLTVFGPQITSPALQTTLTQALYN	240
Db	181	KMQQFVNDQFNKTAQELDCIKIAQGVVELNLYLTETLTVFGPQITSPALKNLTITQALYN	240
Qy	241	LAGGNMVDLLTKLGVNNQLSSLGSLITGNPILYDSQTQLLGIQVTLPSVGNLNNMRA	300
Db	241	LAGGNMVDLLTKLGVNNQLSSLGSLITGNPILYDSQTQLLGIQVTLPSVGNLNNMRA	300
Qy	301	TYLETLSVSTTKGFASALVPKVMKGVSVIEBELDTSYCIETDLDYCTRTVTFPMSPGIY	360
Db	301	TYLETLSVSTTRGFASALVPKVVTVQGVSVIEBELDTSYCIETDLDYCTRTVTFPMSPGIY	360
Qy	361	SCLSGNTSACMSYKTEGALTTPYMTLKGSVIANCKMTTCRCADPPGIIISQNYGEAVSLID	420
Db	361	SCLSGNTSACMSYKTEGALTTPYMTIKGSVIANCKMTTCRCVNPFGIIISQNYGEAVSLID	420
Qy	421	RQSCNVLSLDGTTLRLSGEFDATYQKNISIQDSQVIVTGNLDISTELGNVNNISNALDK	480
Db	421	RQSCNVLSLDGTTLRLSGEFDVYQKNISIQDSQVITGNLDISTELGNVNNISNALNK	480
Qy	481	LEESNKLDKVNVKLTSTTSALITYIVLTIVTSVCGILSLVACLYMYKQAKQKTLWLIG	540
Db	481	LEESNRKLDKVNKLTSTTSALITYIVLTIIISLVFGILSLILACLYMYKQAKQKTLWLIG	540

Db 421 KQCNVLSLGGITLRLSGEFATYQKNISIQDSQVITGNLDISTELGNVNSISNALNK 480
Qy 481 LEESNSKLDKVNKLTSTSLITYIVLTIVLSVCGILSLVACVLMYKQAKQKTLMLG 540
Db 481 LEESNSKLDKVNKLTSTSLITYIVLTIVLSVCGILSLVACVLMYKQAKQKTLMLG 540
Qy 541 NNTLDQMRATTKM 553
Db 541 NNTLDQMRATTKM 553

RESULT 10

S40163
cell fusion protein - Newcastle disease virus
C:Species: Newcastle disease virus
C:Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 24-Nov-1999
C:Accession: S40163
R:Kalinan, A.; Zadori, Z.; Kisari, J.; Fodor, I.
submitted to the EMBL Data Library, May 1993
A:Description: Nucleotide sequence of the hemagglutinin-neuraminidase (HN) gene of newca
A:Reference number: S40163
A:Accession: S40163
A:Status: Preliminary
A:Molecule type: genomic RNA
A:Residues: 1-553 <KAL>
A:Cross-references: EMBL:X71995; NID:9437886; PIDN:CAAS0869.1; PID:9437887
C:Superfamily: parainfluenza virus cell fusion protein

Query Match 94.4%; Score 2602; DB 2; Length 553;
Best Local Similarity 94.4%; Pred. No. 6e-155;
Matches 522; Conservative 11; Mismatches 20; Indels 0; Gaps 0;
Qy 1 MGRSSSTRIPVPLMTVRVALALSCVPTSSLDGRPLAAAGIVVTGKAVNIYSSQTGS 60
Db 1 MRSRSSTRIPVPLMLIIRIALTSLCIRLTSSLDGRPLAAAGIVVTGKAVNIYSSQTGS 60

Qy 61 IIVKLLPNMPKDEKACAKAPLEAYNRTLTLLTPLGDSIRRIQSVTTSGGKQRLIGA 120
Db 61 IIVKLLPNMPKDEKACAKAPLEAYNRTLTLLTPLGDSIRRIQSVTTSGGKQRLIGA 120
Qy 121 IIGGAALGVATAAQITTAASALIQANQNAANILRLKERIAATNEAVHEVTDGLSOLAVAG 180
Db 121 IIGSVLGVATAAQITTAASALIQANQNAANILRLKESIAATNEAAHEVTDGLSOLAVAG 180
Qy 181 KMQQFVNDQFNKTAQELDCIKITQGVGVELNLYLTTELTVFGPQITSPALTQTITQALYN 240
Db 181 KMQQFVNDQFNNTAQELDCIKITQGVGVELNLYLTTELTVFGPQITSPALTQTITQALYN 240
Qy 241 LAGNMNDYLLTKLGVGNQLSSLGSLITGNPILYDSQTQLGQITLPSVGNLNNMRA 300
Db 241 LAGNMNDYLLTKLGVGNQLSSLGSLITGNPILYDSQTQLGQITLPSVGNLNNMRA 300
Qy 301 TYLETSLVSTTKGFASALVPKVMKGVSVIEELDTSYCIETDLDLYCTRIVTFPMSPGIY 360
Db 301 TYLETSLVSTTKGFASALVPKVTQVGSVIEELDTSYCIETDLDLYCTRIVTFPMSPGIY 360
Qy 361 SCLSGNTSACMYKTEGALTTPYMTLKGSVIANCKMTTCRCADPPGIIISQNYGEAVSLID 420
Db 361 SCLSGNTSACMYKTEGALTTPYMTLKGSVIANCKMTTCRCADPPGIIISQNYGEAVSLID 420
Qy 421 ROSCNVLSLDGITLRLSGEFATYQKNISIQDSQVITGNLDISTELGNVNSISNALDK 480
Db 421 RHSCNVLSLDGITLRLSGEFATYQKNISIQDSQVITGNLDISTELGNVNSISNALNK 480
Qy 481 LEESNSKLDKVNKLTSTSLITYIVLTIVLSVCGILSLVACVLMYKQAKQKTLMLG 540
Db 481 LEESNSKLDKVNKLTSTSLITYIVLTIVLSVCGILSLVACVLMYKQAKQKTLMLG 540
Qy 541 NNTLDQMRATTKM 553
Db 541 NNTLDQMRATTKI 553

RESULT 11

S06345
cell fusion glycoprotein precursor - Newcastle disease virus (strain Italian)
N:Contains: fusion glycoprotein F1; fusion glycoprotein F2
C:Species: Newcastle disease virus
C:Date: 30-Jun-1991 #sequence_revision 30-Jun-1991 #text_change 24-Nov-1999
C:Accession: S06345
R:Espion, D.; de Henau, S.; Letellier, C.; Wemmers, C.D.; Brasseur, R.; Young, J.F.; Gros
Arch. Virol. 95, 79-95, 1987
A:Title: Expression at the cell surface of native fusion protein of the Newcastle disease
A:Reference number: S06345; MUID:87240797; PMID:3592986
A:Accession: S06345
A:Molecule type: Genomic RNA
A:Residues: 1-553 <ESP>
A:Cross-references: EMBL:M17710
A:Note: it is uncertain whether Met-1 or Met-14 is the initiator
C:Genetics:
A:Gene: F
C:Superfamily: parainfluenza virus cell fusion protein
C:Keywords: glycoprotein; transmembrane protein
F:1-31/Domain: signal sequence #status predicted <SIG>
F:32-116/Product: fusion glycoprotein F2 #status predicted <P2P>
F:117-553/Product: fusion glycoprotein F1 #status predicted <FLP>
F:495-525/Domain: transmembrane #status predicted <TM>
F:85,191,366,447,471,541/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 94.3%; Score 2599; DB 2; Length 553;
Best Local Similarity 94.4%; Pred. No. 9.2e-155;
Matches 522; Conservative 12; Mismatches 19; Indels 0; Gaps 0;

Qy 1 MGRSSSTRIPVPLMTVRVALALSCVPTSSLDGRPLAAAGIVVTGKAVNIYSSQTGS 60
Db 1 MRSRSSTRIPVPLMLIIRIALTSLCIRLTSSLDGRPLAAAGIVVTGKAVDIYSSQTGS 60
Qy 61 IIVKLLPNMPKDEKACAKAPLEAYNRTLTLLTPLGDSIRRIQSVTTSGGKQRLIGA 120
Db 61 IIVKLLPNMPKDEKACAKAPLEAYNRTLTLLTPLGDSIRRIQSVTTSGGRRQRFIGA 120
Qy 121 IIGGAALGVATAAQITTAASALIQANQNAANILRLKERIAATNEAVHEVTDGLSOLAVAG 180
Db 121 IIGSVLGVATAAQITTAASALIQANQNAANILRLKESIAATNEAVHEVTDGLSOLAVAG 180
Qy 181 KMQQFVNDQFNKTAQELDCIKITQGVGVELNLYLTTELTVFGPQITSPALTQTITQALYN 240
Db 181 KMQQFVNDQFNNTAQELDCIKITQGVGVELNLYLTTELTVFGPQITSPALTQTITQALYN 240
Qy 241 LAGNMNDYLLTKLGVGNQLSSLGSLITGNPILYDSQTQLGQITLPSVGNLNNMRA 300
Db 241 LAGNMNDYLLTKLGVGNQLSSLGSLITGNPILYDSQTQLGQITLPSVGNLNNMRA 300
Qy 301 TYLETSLVSTTKGFASALVPKVMKGVSVIEELDTSYCIETDLDLYCTRIVTFPMSPGIY 360
Db 301 TYLETSLVSTTKGFASALVPKVTQVGSVIEELDTSYCMETDLDLYCTRIVTFPMSPGIY 360
Qy 361 SCLSGNTSACMYKTEGALTTPYMTLKGSVIANCKMTTCRCADPPGIIISQNYGEAVSLID 420
Db 361 SCLSGNTSACMYKTEGALTTPYMTLKGSVIANCKMTTCRCADPPGIIISQNYGEAVSLID 420
Qy 421 ROSCNVLSLDGITLRLSGEFATYQKNISIQDSQVITGNLDISTELGNVNSISNALDK 480
Db 421 RHSCNVLSLDGITLRLSGEFATYQKNISIQDSQVITGNLDISTELGNVNSISNALNK 480
Qy 481 LEESNSKLDKVNKLTSTSLITYIVLTIVLSVCGILSLVACVLMYKQAKQKTLMLG 540
Db 481 LEESNSKLDKVNKLTSTSLITYIVLTIVLSVCGILSLVACVLMYKQAKQKTLMLG 540
Qy 541 NNTLDQMRATTKM 553
Db 541 NNTLDQMRATTKI 553

RESULT 12

A36830

cell fusion glycoprotein precursor - Newcastle disease virus (strain HER/33)
N/Contains: fusion glycoprotein F1; fusion glycoprotein F2

C/Species: Newcastle disease virus

C/Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 16-Jul-1999

C/Accession: A36830

R/Toyoda, T.; Sakaguchi, T.; Hirota, H.; Gotoh, B.; Kuma, K.; Miyata, T.; Nagai, Y.

Virolgy 169, 273-282, 1989

A/Title: Newcastle disease virus evolution. II. Lack of gene recombination in generating

A/Reference number: A46329; MUID:89204899; PMID:2705298

A/Accession: A36830

A/Molecule type: genomic RNA

A/Residues: 1-553 <TOY>

A/Cross-references: GB:M24702; NID:g293937; PIDN:AAA46652.1; PID:g293938

C/Genetics:

A/Gene: F

C/Superfamily: parainfluenza virus cell fusion protein

C/Keywords: glycoprotein; membrane fusion; transmembrane protein

F/1-25/Domain: signal sequence #status predicted <SIG>

F/26-117/Product: cell fusion glycoprotein F2 #status predicted <PF2>

F/118-553/Product: cell fusion glycoprotein F1 #status predicted <FF1>

F/495-528/Domain: transmembrane #status predicted <TMN>

F/85,191,366,447,471/Binding site: carbohydrate (Asn) #status predicted

Query Match 94.2%; Score 2598; DB 1; Length 553;

Best Local Similarity 94.4%; Pred. No. 1.1e-154; Indels 0; Gaps 0;

Matches 522; Conservative 11; Mismatches 20;

QY 1 MGRSRSTRIPVPLMLTVRVALALSCVPTSSLDGRPLAAAGIVVTGDKAVNIYTSQTGS 60

DB 1 MGRSRSTRIPVPPMLIIRIVLTSLCRLTSSLDGRPLAAAGIVVTGDKAVNIYTSQTGS 60

QY 61 IIVKLLPNPKDKEACAKAPLEAYNRTLTLLPLGDSIRRIQESVTTSGGGHQLIGA 120

DB 61 IIVKLLPNPKDKEACAKAPLEAYNRTLTLLPLGDSIRRIQESVTTSGGRQRRFIGA 120

QY 121 IIGGAALGVATAAQITAAASALIQANQANAIILRLKERIAATNEAVHEVTDGSLAVAVG 180

DB 121 IIGSVALGVATAAQITAAASALIQANQANAIILRLKESIAATNEAVHEVTDGSLAVAVG 180

QY 181 KMQQFVNDQFNNTAQELDCIKITQQVGVNELNLYLTETLTVFGPQITSPALTIQALYN 240

DB 181 KMQQFVNDQFNNTAQELDCIKITQQVGVNELNLYLTETLTVFGPQITSPALTIQALYN 240

QY 241 LAGGNMDYLLTKLGVGNQNLSSLGSLITGNPILYDSQTQLLGIQVTLPSVGNLNMRA 300

DB 241 LAGGNMDYLLTKLGVGNQNLSSLGSLITGNPILYDSQTQLLGIQVTLPSVGNLNMRA 300

QY 301 TYLETLSVTTKGFASALVPKVMKGVSVIEELDTSYCIETDLDTCTRIVTFPMSPGIY 360

DB 301 TYLETLSVTTKGFASALVPKVMKGVSVIEELDTSYCIETDLDTCTRIVTFPMSPGIY 360

QY 361 SCLSGNTSACMSKTEGALTTPYMTLKGSVIANCKMTTCRCADPPGIIISQNYGEAVSLID 420

DB 361 SCLSGNTSACMSKTEGALTTPYMTLKGSVIANCKMTTCRCADPPGIIISQNYGEAVSLID 420

QY 421 ROSCNVSLDGLTIRLSGEFDATYQKNISIQDSQVITGNLDISTELGNVNNISNALDK 480

DB 421 RHSCNVSLDGLTIRLSGEFDATYQKNISIQDSQVITGNLDISTELGNVNNISNALNK 480

QY 481 LEESNKLKVNKLTSTSAITYIVLTIVSLVCGILSLVLACYLWYKQAKOQKTLWLWG 540

DB 481 LEESNKLKVNKLTSTSAITYIVLTIVSLVCGILSLVLACYLWYKQAKOQKTLWLWG 540

QY 541 NNTLDQMRATTKM 553

DB 541 NNTLDQMRATTKI 553

RESULT 13

G46329

cell fusion glycoprotein precursor - Newcastle disease virus (strain TEX/48)

N/Contains: fusion glycoprotein F1; fusion glycoprotein F2

C/Species: Newcastle disease virus

C/Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 16-Jul-1999

C/Accession: G46329; S11266

R/Toyoda, T.; Sakaguchi, T.; Hirota, H.; Gotoh, B.; Kuma, K.; Miyata, T.; Nagai, Y.

Virolgy 169, 273-282, 1989

A/Title: Newcastle disease virus evolution. II. Lack of gene recombination in generating

A/Reference number: A46329; MUID:89204899; PMID:2705298

A/Accession: G46329

A/Molecule type: genomic RNA

A/Residues: 1-553 <TOY>

A/Cross-references: GB:M24698; NID:g293931; PIDN:AAA46649.1; PID:g293932

R/Richardson, C.D.; Scheid, A.; Chopin, P.W.

Virolgy 105, 205-222, 1980

A/Title: Specific inhibition of paramyxovirus and myxovirus replication by oligopeptide:

A/Reference number: S11266; MUID:81016739; PMID:7414950

A/Accession: S11266

A/Molecule type: protein

A/Residues: 117-136 <RIC>

C/Genetics:

A/Gene: F

C/Superfamily: parainfluenza virus cell fusion protein

C/Keywords: glycoprotein; membrane fusion; transmembrane protein

F/1-25/Domain: signal sequence #status predicted <SIG>

F/26-117/Product: cell fusion glycoprotein F2 #status predicted <PF2>

F/118-553/Product: cell fusion glycoprotein F1 #status predicted <FF1>

F/495-528/Domain: transmembrane #status predicted <TMN>

F/85,191,366,447,471/Binding site: carbohydrate (Asn) #status predicted

Query Match 94.1%; Score 2593; DB 1; Length 553;

Best Local Similarity 93.1%; Pred. No. 2.2e-154; Indels 0; Gaps 0;

Matches 535; Conservative 19; Mismatches 19;

QY 1 MGRSRSTRIPVPLMLTVRVALALSCVPTSSLDGRPLAAAGIVVTGDKAVNIYTSQTGS 60

DB 1 MGRSRSTRIPVPLMLTVRVALALSCVPTSSLDGRPLAAAGIVVTGDKAVNIYTSQTGS 60

QY 61 IIVKLLPNPKDKEACAKAPLEAYNRTLTLLPLGDSIRRIQESVTTSGGGHQLIGA 120

DB 61 IIVKLLPNPKDKEACAKAPLEAYNRTLTLLPLGDSIRRIQESVTTSGGRQRRFIGA 120

QY 121 IIGGAALGVATAAQITAAASALIQANQANAIILRLKERIAATNEAVHEVTDGSLAVAVG 180

DB 121 IIGSVALGVATAAQITAAASALIQANQANAIILRLKESIAATNEAVHEVTDGSLAVAVG 180

QY 181 KMQQFVNDQFNNTAQELDCIKITQQVGVNELNLYLTETLTVFGPQITSPALTIQALYN 240

DB 181 KMQQFVNDQFNNTAQELDCIKITQQVGVNELNLYLTETLTVFGPQITSPALTIQALYN 240

QY 241 LAGGNMDYLLTKLGVGNQNLSSLGSLITGNPILYDSQTQLLGIQVTLPSVGNLNMRA 300

DB 241 LAGGNMDYLLTKLGVGNQNLSSLGSLITGNPILYDSQTQLLGIQVTLPSVGNLNMRA 300

QY 301 TYLETLSVTTKGFASALVPKVMKGVSVIEELDTSYCIETDLDTCTRIVTFPMSPGIY 360

DB 301 TYLETLSVTTKGFASALVPKVMKGVSVIEELDTSYCIETDLDTCTRIVTFPMSPGIY 360

QY 361 SCLSGNTSACMSKTEGALTTPYMTLKGSVIANCKMTTCRCADPPGIIISQNYGEAVSLID 420

DB 361 SCLSGNTSACMSKTEGALTTPYMTLKGSVIANCKMTTCRCADPPGIIISQNYGEAVSLID 420

QY 421 ROSCNVSLDGLTIRLSGEFDATYQKNISIQDSQVITGNLDISTELGNVNNISNALDK 480

DB 421 RHSCNVSLDGLTIRLSGEFDATYQKNISIQDSQVITGNLDISTELGNVNNISNALNK 480

QY 481 LEESNKLKVNKLTSTSAITYIVLTIVSLVCGILSLVLACYLWYKQAKOQKTLWLWG 540

DB 481 LEESNKLKVNKLTSTSAITYIVLTIVSLVCGILSLVLACYLWYKQAKOQKTLWLWG 540

QY 541 NNTLDQMRATTKM 553

DB 541 NNTLDQMRATTKM 553

RESULT 14

B36930
 N:Contains: fusion glycoprotein precursor - Newcastle disease virus (strain ITA/45)
 C:Species: fusion glycoprotein F1; fusion glycoprotein F2
 C:Accession: B36830
 C:Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 07-May-1999
 R:Toyoda, T.; Sakaguchi, T.; Hirota, H.; Gotoh, B.; Kuma, K.; Miyata, T.; Nagai, Y.
 A:Title: Newcastle disease virus evolution. II. Lack of gene recombination in generating
 A:Reference number: A46329; MUID:89204898; PMID:2705298
 A:Accession: B36830
 A:Molecule type: genomic RNA
 A:Residues: 1-553 <TOY>
 A:Gene: F
 C:Cross-references: GB:M24703
 C:Genetics:
 C:Superfamily: parainfluenza virus cell fusion protein
 C:Keywords: Glycoprotein; membrane fusion; transmembrane protein
 F:1-25/Domain: signal sequence #status predicted <SIG>
 F:36-117/Product: cell fusion glycoprotein F2 #status predicted <FP2>
 F:118-553/Product: cell fusion glycoprotein F1 #status predicted <FP1>
 F:495-528/Domain: transmembrane #status predicted <TMN>
 F:85,191,366,447,471/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match	94.0%;	Score 2592;	DB 1;	Length 553;
Best Local Similarity	94.2%;	Pred. No. 2.5e-154;	Mismatches 20;	Indels 0; Gaps 0;
Matches	521;	Conservative	12;	

Qy	1	MGRSSSTRIPVPLMLTVRVALALSCVPTSSLDGRPLAAAGIVVTGKAVNIYTSSTQGS	60
Db	1	MGRSSSTRIPVPLMLTVRVALALSCVPTSSLDGRPLAAAGIVVTGKAVNIYTSSTQGS	60
Qy	61	IIIVKLLPNMPKDEACAKAPLEAYNRITLTLLPLGDSIRRIQESVTTSGGKQRLIGA	120
Db	61	IIIVKLLPNMPKDEACAKAPLEAYNRITLTLLPLGDSIRRIQESVTTSGGKQRLIGA	120
Qy	121	IIGGAALGVATAAQITAAALIQANNAANILRLKERIAATNEAVHEVTDGLSOLAVAG	180
Db	121	IIGSVLGVATPAQITAAALIQANNAANILRLKESIAATNEAVHEVTDGLSOLAVAG	180
Qy	181	KMOQFVNDQFNKTAQELDCIKITQQGVVELNLYLTETLTVFGPOITSPALTLTIOALYN	240
Db	181	KMOQFVNDQFNNTAQQLDCIKITQQGVVELNLYLTETLTVFGPOITSPALTLTIOALYN	240
Qy	241	LAGNMDYLLTKLGVGNQLSSGLITGNPILYDSOTQLLGIQVTLPSVGNLNMRA	300
Db	241	LAGNMDYLLTKLGVGNQLSSGLITGNPILYDSOTQLLGIQVTLPSVGNLNMRA	300
Qy	301	TYLETLSVSTTKGFASALVPKVMKGVSVIEELDTSCYIETDLDLYCTRIVTFPMSPGIY	360
Db	301	TYLETLSVSTTKGFASALVPKVMKGVSVIEELDTSCYIETDLDLYCTRIVTFPMSPGIY	360
Qy	361	SCLSGNTSACMSYKTEGALTTPYMTLKGSVIANCKMTTCRCADPPGIISQNYGAVSLID	420
Db	361	SCLSGNTSACMSYKTEGALTTPYMTLKGSVIANCKMTTCRCADPPGIISQNYGAVSLID	420
Qy	421	RQSCNVLSDGITLRLSGEFDATYQKNISIQDSQVITVGNLDISTELGNVNNISNALDK	480
Db	421	RHSNCNVLSDGITLRLSGEFDATYQKNISIQDSQVITVGNLDISTELGNVNNISNALDK	480
Qy	481	LEESNKLDKVNVKLTSTALITYIVLTIVSLVCGILSLVACVLMYKQKQAQKTLWLIG	540
Db	481	LEESNKLDKVNVKLTSTALITYIVLTIVSLVCGILSLVACVLMYKQKQAQKTLWLIG	540
Qy	541	NTTLDQMRATTKM	553
Db	541	NTTLDQMRATTKI	553

RESULT 15

VANZGB
 cell fusion glycoprotein precursor - Newcastle disease virus (strain Texas G.B.)

N:Contains: fusion glycoprotein F1; fusion glycoprotein F2
 C:Species: Newcastle disease virus
 C:Date: 31-Dec-1989 #sequence_revision 31-Dec-1989 #text_change 25-Oct-1996
 C:Accession: B29201
 R:Schaper, U.M.; Fuller, F.J.; Ward, M.D.W.; Mehrotra, Y.; Stone, H.O.; Stripp, B.R.; D
 A:Title: Nucleotide sequence of the envelope protein genes of a highly virulent, neurot
 A:Reference number: A94379; MUID:88265873; PMID:3388773
 A:Accession: B29201
 A:Molecule type: mRNA
 A:Residues: 1-553 <SCH>
 A:Experimental source: strain Texas G.B.
 C:Genetics:
 A:Gene: F
 C:Superfamily: parainfluenza virus cell fusion protein
 C:Keywords: Glycoprotein; membrane fusion; transmembrane protein
 F:1-31/Domain: signal sequence #status predicted <SIG>
 F:32-111/Product: cell fusion glycoprotein F2 #status predicted <FP2>
 F:112-116/Region: cleavage processing #status predicted
 F:117-553/Product: cell fusion glycoprotein F1 #status predicted <FP1>
 F:9,85,191,366,447,471,541/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match	93.9%;	Score 2589;	DB 1;	Length 553;
Best Local Similarity	92.9%;	Pred. No. 3.9e-154;	Mismatches 20;	Indels 0; Gaps 0;
Matches	514;	Conservative	19;	

Qy	1	MGRSSSTRIPVPLMLTVRVALALSCVPTSSLDGRPLAAAGIVVTGKAVNIYTSSTQGS	60
Db	1	MGRPSPTKPTPMLTVRVALVIGICIPANSIDGRPLAAAGIVVTGKAVNIYTSSTQGS	60
Qy	61	IIIVKLLPNMPKDEACAKAPLEAYNRITLTLLPLGDSIRRIQESVTTSGGKQRLIGA	120
Db	61	IIIVKLLPNLPKDEACAKAPLDAYNRITLTLLPLGDSIRRIQESVTTSGGRQKRFIGA	120
Qy	121	IIGGAALGVATAAQITAAALIQANNAANILRLKERIAATNEAVHEVTDGLSOLAVAG	180
Db	121	IIGVALGVATAAQITAAALIQAKNAANILRLKESIAATNEAVHEVTDGLSOLAVAG	180
Qy	181	KMOQFVNDQFNKTAQELDCIKITQQGVVELNLYLTETLTVFGPOITSPALTLTIOALYN	240
Db	181	KMOQFVNDQFNKTAQESGIRIAQGVVELNLYLTETLTVFGPOITSPALNKLTIOALYN	240
Qy	241	LAGNMDYLLTKLGVGNQLSSGLITGNPILYDSOTQLLGIQVTLPSVGNLNMRA	300
Db	241	LAGNMDYLLTKLGVGNQLSSGLITGNPILYDSOTQLLGIQVTLPSVGNLNMRA	300
Qy	301	TYLETLSVSTTKGFASALVPKVMKGVSVIEELDTSCYIETDLDLYCTRIVTFPMSPGIY	360
Db	301	TYLETLSVSTTRGFASALVPKVMKGVSVIEELDTSCYIETDLDLYCTRIVTFPMSPGIY	360
Qy	361	SCLSGNTSACMSYKTEGALTTPYMTLKGSVIANCKMTTCRCADPPGIISQNYGAVSLID	420
Db	361	SCLSGNTSACMSYKTEGALTTPYMTIRKSVIANCKMTTCRCVNPFGIISQNYGAVSLID	420
Qy	421	RQSCNVLSDGITLRLSGEFDATYQKNISIQDSQVITVGNLDISTELGNVNNISNALDK	480
Db	421	KQSCNVLSDGITLRLSGEFDATYQKNISIQDSQVITVGNLDISTELGNVNNISNALNK	480
Qy	481	LEESNKLDKVNVKLTSTALITYIVLTIVSLVCGILSLVACVLMYKQKQAQKTLWLIG	540
Db	481	LEESNKLDKVNVKLTSTALITYIVLTIVSLVFGILSLVACVLMYKQKQAQKTLWLIG	540
Qy	541	NTTLDQMRATTKM	553
Db	541	NTTLDQMRATTKM	553

Search completed: April 18, 2004, 02:33:33
 Job time : 48 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: April 18, 2004, 01:19:18 ; Search time 46 Seconds
(without alignments)
1156.389 Million cell updates/sec

Title: US-10-725-841-2
Perfect score: 2757
Sequence: 1 MGRSSTRIPVPLMLTVRVA.....KTLMLGNLTLDQMRATTKM 553

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 78:*

1: Pir1:*

2: Pir2:*

3: Pir3:*

4: Pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2724	98.8	553	1 VGNZU1	cell fusion glycop
2	2724	98.8	553	1 A46329	cell fusion glycop
3	2691	97.6	553	2 S23621	gene F protein - N
4	2684	97.4	553	1 B46329	cell fusion glycop
5	2658	96.4	553	2 S38785	gene F protein - N
6	2625	95.2	553	1 H46329	cell fusion glycop
7	2622	95.1	553	1 D46329	cell fusion glycop
8	2606	94.5	553	1 VGNZTE	cell fusion glycop
9	2603	94.4	553	1 VGNZNV	cell fusion glycop
10	2602	94.4	553	2 S40163	cell fusion glycop
11	2599	94.3	553	2 S06345	cell fusion glycop
12	2598	94.2	553	1 A36830	cell fusion glycop
13	2593	94.1	553	1 A36830	cell fusion glycop
14	2592	94.0	553	1 B36830	cell fusion glycop
15	2589	93.9	553	1 VGNZGB	cell fusion glycop
16	2588	93.9	553	1 B46329	cell fusion glycop
17	2585	93.8	553	1 I46329	cell fusion glycop
18	2579	93.5	553	1 VGNZND	cell fusion glycop
19	2575	93.4	553	2 S38784	gene F protein - N
20	2555	92.7	553	2 S23622	gene F protein - N
21	2554	92.6	553	2 S23620	F protein - N
22	2549	92.5	553	2 S38786	gene F protein - N
23	1018.5	36.9	534	2 A37483	F protein - Muraya
24	717	26.0	529	1 VGNZSP	cell fusion glycop
25	712.5	25.8	538	1 VGNZMM	cell fusion glycop
26	712.5	25.8	538	2 S52472	cell fusion protei
27	704	25.5	538	1 VGNZMS	cell fusion glycop
28	704	25.5	551	1 VGNZP2	cell fusion glycop
29	701.5	25.4	538	1 VGNZMU	cell fusion glycop

ALIGNMENTS

RESULT 1

VGNZU1
cell fusion glycoprotein precursor - Newcastle disease virus (strains Ulster and ULS/e
N; Contains: fusion glycoprotein F1; fusion glycoprotein F2
C:Species: Newcastle disease virus
C:Date: 30-Jun-1989 #sequence_revision 30-Jun-1989 #text_change 16-Jun-2000
C:Accession: A29823; C46329
R:Millar, N.S.; Chambers, P.; Emerson, P.T.
J. Gen. Virol. 69, 613-620, 1988
A:Title: Nucleotide sequence of the fusion and haemagglutinin-neuraminidase glycoprote
ns.
A:Reference number: A92799; UID:88171450; PMID:3351479
A:Accession: A29823
A:Molecule type: mRNA
A:Residues: 1-553 <MIL>
A:Cross-references: GB:D00243; NID:G222174; PIDN:BA00173.1; PID:G222175
A:Experimental source: strain Ulster
R:Toyoda, T.; Sakaguchi, T.; Hirota, H.; Gotoh, B.; Kuma, K.; Miyata, T.; Nagai, Y.
Virolgy 169, 273-282, 1989
A:Title: Newcastle disease virus evolution. II. Lack of gene recombination in generati
A:Reference number: A46329; UID:89204898; PMID:2705298
A:Accession: C46329
A:Molecule type: genomic RNA
A:Residues: 1-553 <TOY>
A:Cross-references: GB:M24694; NID:G293923; PIDN:AAA46645.1; PID:G293924
A:Experimental source: strain ULS/67
C:Genetics:
A:Gene: F
C:Superfamily: parainfluenza virus cell fusion protein
C:Keywords: glycoprotein; membrane fusion; transmembrane protein
F:1-25/Domain: signal sequence #status predicted <SIG>
F:26-117/Product: cell fusion glycoprotein F2 #status predicted <PF2>
F:118-553/Product: cell fusion glycoprotein F1 #status predicted <FPI>
F:495-528/Domain: transmembrane #status predicted <TMN>
F:85,191,366,447,471/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 98.8%; Score 2724; DB 1; Length 553;

Best Local Similarity 99.1%; Pred. No. 1.4e-162;

Matches 548; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy 1 MGRSSTRIPVPLMLTVRVALALSCVPTSSLDGRPLAAGIVVTGKAVNIYTSOTGS 60

Db 1 MGRSSTRIPVPLMLTVRVALALSCVPTSSLDGRPLAAGIVVTGKAVNIYTSOTGS 60

Qy 61 IIVKLLPNMPKDEACAKAPLEAYNRTLTLLPLGDSIRRIQESVTTSGGKQRLIGA 120

Db 61 IIVKLLPNMPKDEACAKAPLEAYNRTLTLLPLGDSIRRIQESVTTSGGKQRLIGA 120

Qy 121 IIGGALGVATAAQITAAASALIOANQNAANILRKERIAATNEAVHEVTDGLSOLAVAG 180

Db 121 IIGGALGVATAAQITAAASALILANQNAANILRKESIAATNEAVHEVTDGLSOLAVAG 180

QY 181 KMQQFVNDQFNKTAQELDCIKITQOVGVNELNLYLTETLVFGPQITSPALQTQALYN 240
DB |||||
QY 181 KMQQFVNDQFNKTAQELDCIKITQOVGVNELNLYLTETLVFGPQITSPALQTQALYN 240
DB |||||
QY 241 LAGGNDYLLTKLGVGNQSLIGSLITGNPILYDSQTQLLGIQVTLPSVGNLNNMRA 300
DB |||||
QY 241 LAGGNDYLLTKLGVGNQSLIGSLITGNPILYDSQTQLLGIQVTLPSVGNLNNMRA 300
DB |||||
QY 301 TYLETLSVSTTKGFASALVPKVMKVGSVIBELDTSYCIETDLDLYCTRIVTFPMSPGIY 360
DB |||||
QY 301 TYLETLSVSTTKGFASALVPKVMKVGSVIBELDTSYCIETDLDLYCTRIVTFPMSPGIY 360
DB |||||
QY 361 SCLSGNTSACMSKTEGALTTPYMTLKGSVIANCKMTTCRCADPPGIISQNYGEAVSLID 420
DB |||||
QY 361 SCLSGNTSACMSKTEGALTTPYMTLKGSVIANCKMTTCRCADPPGIISQNYGEAVSLID 420
DB |||||
QY 421 RQSCNVLSLDGTTLRSLGEFDATYQKNISIQDSQVIVTGNLDISTELGNVNNISNALDK 480
DB |||||
QY 421 RQSCNVLSLDGTTLRSLGEFDATYQKNISIQDSQVIVTGNLDISTELGNVNNISNALDK 480
DB |||||
QY 481 LEESNSKLDKVNKLSTSTALITYIVLTVISLVCGLISLVACYLKYKAKOQKTLMLG 540
DB |||||
QY 481 LEESNSKLDKVNKLSTSTALITYIVLTVISLVCGLISLVACYLKYKAKOQKTLMLG 540
DB |||||
QY 541 NNTLDQMRATTKM 553
DB |||||
QY 541 NNTLDQMRATTKM 553
DB |||||

RESULT 2

A46329
cell fusion glycoprotein precursor - Newcastle disease virus (strain D26/76)
N:Contains: fusion glycoprotein F1; fusion glycoprotein F2
C:Species: Newcastle disease virus
C:Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 16-Jul-1999
R:Toyoda, T.; Sakaguchi, T.; Hirota, H.; Gotoh, B.; Kuma, K.; Miyata, T.; Nagai, Y.
Virology 169, 273-282, 1989
A:Title: Newcastle disease virus evolution. II. Lack of gene recombination in generating
A:Reference number: A46329; UID:89204898; PMID:2705298
A:Accession: A46329
A:Molecule type: Genomic RNA
A:Residues: 1-553 <TOY>
A:Cross-references: GB:M24692; NID:G293919; PIDN:AAA46643.1; PID:G293920
C:Genetics:
A:Gene: F
C:Superfamily: parainfluenza virus cell fusion protein
C:Keywords: Glycoprotein; membrane fusion; transmembrane protein
F1-25/Domain: signal sequence #status predicted <SIG>
F126-117/Product: cell fusion glycoprotein F2 #status predicted <PF2>
F118-553/Product: cell fusion glycoprotein F1 #status predicted <PF1>
F495-528/Domain: transmembrane #status predicted <TMN>
F185,191,366,447,471/Binding site: carbohydrate (Asn) #status predicted

Query Match 98.8%; Score 2724; DB 1; Length 553;
Best Local Similarity 98.4%; Pred. No. 1.4e-162;
Matches 544; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

QY 1 MGSRSSTRIPVPLMLTVRVALSVCVPTSSLDGRPLAAAGIVTGDKAIVYTSSQTS 60
DB |||||
QY 1 MGSRSSTRIPVPLMLTVRIMALSVCVPTSSLDGRPLAAAGIVTGDKAIVYTSSQTS 60
DB |||||
QY 61 IIVKLLPNPKDKEACAKAPLEAYNRTLTLLTPLGDSIRRIQESVTTSGGKQGRLLGA 120
DB |||||
QY 61 IIVKLLPNPKDKEACAKAPLEAYNRTLTLLTPLGDSIRRIQESVTTSGGKQGRLLGA 120
DB |||||
QY 121 IIGGAALGVATAAQITAAALIOANQANANILRLKERIAATNEAVEHVTGSLQAVAVG 180
DB |||||
QY 121 IIGGVALGVATAAQITAAALIOANQANANILRLKESIAATNEAVEHVTGSLQAVAVG 180
DB |||||
QY 181 KMQQFVNDQFNKTAQELDCIKITQOVGVNELNLYLTETLVFGPQITSPALQTQALYN 240
DB |||||
QY 181 KMQQFVNDQFNKTAQELDCIKITQOVGVNELNLYLTETLVFGPQITSPALQTQALYN 240
DB |||||

QY 241 LAGGNDYLLTKLGVGNQSLIGSLITGNPILYDSQTQLLGIQVTLPSVGNLNNMRA 300
DB |||||
QY 241 LAGGNDYLLTKLGVGNQSLIGSLITGNPILYDSQTQLLGIQVTLPSVGNLNNMRA 300
DB |||||
QY 301 TYLETLSVSTTKGFASALVPKVMKVGSVIBELDTSYCIETDLDLYCTRIVTFPMSPGIY 360
DB |||||
QY 301 TYLETLSVSTTKGFASALVPKVMKVGSVIBELDTSYCIETDLDLYCTRIVTFPMSPGIY 360
DB |||||
QY 361 SCLSGNTSACMSKTEGALTTPYMTLKGSVIANCKMTTCRCADPPGIISQNYGEAVSLID 420
DB |||||
QY 361 SCLSGNTSACMSKTEGALTTPYMTLKGSVIANCKMTTCRCADPPGIISQNYGEAVSLID 420
DB |||||
QY 421 RQSCNVLSLDGTTLRSLGEFDATYQKNISIQDSQVIVTGNLDISTELGNVNNISNALDK 480
DB |||||
QY 421 RQSCNVLSLDGTTLRSLGEFDATYQKNISIQDSQVIVTGNLDISTELGNVNNISNALDK 480
DB |||||
QY 481 LEESNSKLDKVNKLSTSTALITYIVLTVISLVCGLISLVACYLKYKAKOQKTLMLG 540
DB |||||
QY 481 LEESNSKLDKVNKLSTSTALITYIVLTVISLVCGLISLVACYLKYKAKOQKTLMLG 540
DB |||||
QY 541 NNTLDQMRATTKM 553
DB |||||
QY 541 NNTLDQMRATTKM 553
DB |||||

RESULT 3

S23621
gene F protein - Newcastle disease virus
C:Species: Newcastle disease virus
C:Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 25-Oct-1996
C:Accession: S23621
R:Pritzer, E.; Kuroda, K.; Garten, W.; Nagai, Y.; Klenk, H.D.
Virus Res. 15, 237-242, 1990
A:Title: A host range mutant of Newcastle disease virus with an altered cleavage site
A:Reference number: S23620; UID:90261333; PMID:2188464
A:Accession: S23621
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-553 <PRI>
A:Cross-references: EMBL:Z12110
C:Superfamily: parainfluenza virus cell fusion protein

Query Match 97.6%; Score 2691; DB 2; Length 553;
Best Local Similarity 98.2%; Pred. No. 1.7e-160;
Matches 543; Conservative 1; Mismatches 9; Indels 0; Gaps 0;

QY 1 MGSRSSTRIPVPLMLTVRVALSVCVPTSSLDGRPLAAAGIVTGDKAIVYTSSQTS 60
DB |||||
QY 1 MGSRSSTRIPVPLMLTVRVALSVCVPTSSLDGRPLAAAGIVTGDKAIVYTSSQTS 60
DB |||||
QY 61 IIVKLLPNPKDKEACAKAPLEAYNRTLTLLTPLGDSIRRIQESVTTSGGKQGRLLGA 120
DB |||||
QY 61 IIVKLLPNPKDKEACAKAPLEAYNRTLTLLTPLGDSIRRIQESVTTSGGKQGRLLGA 120
DB |||||
QY 121 IIGGAALGVATAAQITAAALIOANQANANILRLKERIAATNEAVEHVTGSLQAVAVG 180
DB |||||
QY 121 IIGGAALGVATAAQITAAALIOANQANANILRLKESIAATNEAVEHVTGSLQAVAVG 180
DB |||||
QY 181 KMQQFVNDQFNKTAQELDCIKITQOVGVNELNLYLTETLVFGPQITSPALQTQALYN 240
DB |||||
QY 181 KMQQFVNDQFNKTAQELDCIKITQOVGVNELNLYLTETLVFGPQITSPALQTQALYN 240
DB |||||
QY 241 LAGGNDYLLTKLGVGNQSLIGSLITGNPILYDSQTQLLGIQVTLPSVGNLNNMRA 300
DB |||||
QY 241 LAGGNDYLLTKLGVGNQSLIGSLITGNPILYDSQTQLLGIQVTLPSVGNLNNMRA 300
DB |||||
QY 301 TYLETLSVSTTKGFASALVPKVMKVGSVIBELDTSYCIETDLDLYCTRIVTFPMSPGIY 360
DB |||||
QY 301 TYLETLSVSTTKGFASARVPKVVTVQVSGVIGELDTSYCIETDLDLYCTRIVTFPMSPGIY 360
DB |||||
QY 361 SCLSGNTSACMSKTEGALTTPYMTLKGSVIANCKMTTCRCADPPGIISQNYGEAVSLID 420
DB |||||

Db 361 SCLSGNTSACMYSTEGALTPPYMTLKGSVIANCKMTTCRCADPPGIIISQNYGEAVSLID 420
QY 421 RQSCNVSLDGIITRLSGEFDATYQKNISIQDSQVITVGNLDISTELGNVNNISNALDK 480
Db 421 RQSCNVSLDGIITRLSGEFDATYQKNISIQDSQVITVGNLDISTELGNVNNISNALDK 480
QY 481 LEESNKLKVNKLTSTSTALITYIVLTIVISLVCGILSLVLACLYMYKQKAOQKTLILWG 540
Db 481 LEESNKLKVNKLTSTSTALITYIVLTIVISLVCGILSLVLACLYMYKQKAOQKTLILWG 540
QY 541 NNTLDQMRATTM 553
Db 541 NNTLDQMRATTM 553

RESULT 4
B46329
cell fusion glycoprotein precursor - Newcastle disease virus (strain Que/66)
C;Species: fusion glycoprotein F1; fusion glycoprotein F2
N;Contains: Newcastle disease virus
C;Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 16-Jul-1999
R;Accession: B46329
R;Toyoda, T.; Sakaguchi, T.; Hirota, H.; Gotoh, B.; Kuma, K.; Miyata, T.; Nagai, Y.
Virology 169, 273-282, 1989
A;Title: Newcastle disease virus evolution. II. Lack of gene recombination in generating
A;Reference number: A46329; MUID:99204898; PMID:2705298
A;Accession: B46329
A;Molecule type: genomic RNA
A;Residues: 1-553 <TOY>
A;Cross-references: GB:M24693; NID:g293921; PIDN:AAA46644.1; PID:g293922
C;Genetics:
A;Gene: F
C;Superfamily: parainfluenza virus cell fusion protein
C;Keywords: glycoprotein; membrane fusion; transmembrane protein
F;1-25/Domain: signal sequence #status predicted <SIG>
F;26-117/Product: cell fusion glycoprotein F2 #status predicted <FF2>
F;118-553/Product: cell fusion glycoprotein F1 #status predicted <FF1>
F;495-528/Domain: transmembrane #status predicted <TMN>
F;85,191,366,447,471/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 97.4%; Score 2684; DB 1; Length 553;
Best Local Similarity 97.3%; Pred. No. 4.5e-160;
Matches 538; Conservative 7; Mismatches 8; Indels 0; Gaps 0;

QY 1 MGSRSSTRIPVPLMLTVRVVALALSCVPTSSLDGRPLAAGIVTGDKAVNIYTSQTGS 60
Db 1 MGSRSSTRIPVPLMLTVRVVALALSCVPTSSLDGRPLAAGIVTGDKAVNIYTSQTGS 60
QY 61 IIVKLLPNMPKDEACAKAPLEAYNRTLTLLPLGDSIRRIQESVTTSGGKQGRLLGA 120
Db 61 IIVKLLPNMPKDEACAKAPLEAYNRTLTLLPLGDSIRRIQESVTTSGGKQGRLLGA 120
QY 121 IIGGAALGVATAAQITAAASALIQANQNAANILRLKERIAATNEAVHEVTDGLSOLAVAG 180
Db 121 IIGGAALGVATAAQITAAASALIQANQNAANILRLKERIAATNEAVHEVTDGLSOLAVAG 180
QY 181 KMQOFVNDQNKTAQELDCIKITQOVGVENLXLTELTTVFGPOITSPALTIQALYN 240
Db 181 KMQOFVNDQNKTAQELDCIKITQOVGVENLXLTELTTVFGPOITSPALTIQALYN 240
QY 241 LAGNNDYLLTKLGVGNQNLSSGLITGNPILYDSQTLGLGIQVTLPSVGNLNNMRA 300
Db 241 LAGNNDYLLTKLGVGNQNLSSGLITGNPILYDSQTLGLGIQVTLPSVGNLNNMRA 300
QY 301 TYLETLSVSTTKGFASALVPKVMKGVSVIEELDTSCYIEFDLXYCTRIVTFPMSPGIY 360
Db 301 TYLETLSVSTTKGFASALVPKVMKGVSVIEELDTSCYIEFDLXYCTRIVTFPMSPGIY 360
QY 361 SCLSGNTSACMYSTEGALTPPYMTLKGSVIANCKMTTCRCADPPGIIISQNYGEAVSLID 420
Db 361 SCLSGNTSACMYSTEGALTPPYMTLKGSVIANCKMTTCRCADPPGIIISQNYGEAVSLID 420
QY 421 RQSCNVSLDGIITRLSGEFDATYQKNISIQDSQVITVGNLDISTELGNVNNISNALDK 480
Db 421 RQSCNVSLDGIITRLSGEFDATYQKNISIQDSQVITVGNLDISTELGNVNNISNALDK 480
QY 481 LEESNKLKVNKLTSTSTALITYIVLTIVISLVCGILSLVLACLYMYKQKAOQKTLILWG 540
Db 481 LEESNKLKVNKLTSTSTALITYIVLTIVISLVCGILSLVLACLYMYKQKAOQKTLILWG 540
QY 541 NNTLDQMRATTM 553
Db 541 NNTLDQMRATTM 553

Db 421 RQSCNVSLDGIITRLSGEFDATYQKNISIQDSQVITVGNLDISTELGNVNNISNALDK 480
QY 481 LEESNKLKVNKLTSTSTALITYIVLTIVISLVCGILSLVLACLYMYKQKAOQKTLILWG 540
Db 481 LEESNKLKVNKLTSTSTALITYIVLTIVISLVCGILSLVLACLYMYKQKAOQKTLILWG 540
QY 541 NNTLDQMRATTM 553
Db 541 NNTLDQMRATTM 553

RESULT 5
S38785
Gene F protein - Newcastle disease virus
C;Species: Newcastle disease virus
C;Date: 06-Feb-1995 #sequence_revision 06-Feb-1995 #text_change 20-Sep-1999
C;Accession: S38785
R;Garten, W.D.
submitted to the EMBL Data Library, May 1992
A;Reference number: S22083
A;Accession: S38785
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-553 <CAR>
A;Cross-references: EMBL:Z12110; NID:g60658; PIDN:CAA78095.1; PID:g60659
C;Superfamily: parainfluenza virus cell fusion protein

Query Match 96.4%; Score 2658; DB 2; Length 553;
Best Local Similarity 96.9%; Pred. No. 1.9e-158;
Matches 536; Conservative 2; Mismatches 15; Indels 0; Gaps 0;

QY 1 MGSRSSTRIPVPLMLTVRVVALALSCVPTSSLDGRPLAAGIVTGDKAVNIYTSQTGS 60
Db 1 MGSRSSTRIPVPLMLTVRVVALALSCVPTSSLDGRPLAAGIVTGDKAVNIYTSQTGS 60
QY 61 IIVKLLPNMPKDEACAKAPLEAYNRTLTLLPLGDSIRRIQESVTTSGGKQGRLLGA 120
Db 61 IIVKLLPNMPKDEACAKAPLEAYNRTLTLLPLGDSIRRIQESVTTSGGKQGRLLGA 120
QY 121 IIGGAALGVATAAQITAAASALIQANQNAANILRLKERIAATNEAVHEVTDGLSOLAVAG 180
Db 121 IIGGAALGVATAAQITAAASALIQANQNAANILRLKERIAATNEAVHEVTDGLSOLAVAG 180
QY 181 KMQOFVNDQNKTAQELDCIKITQOVGVENLXLTELTTVFGPOITSPALTIQALYN 240
Db 181 KMQOFVNDQNKTAQELDCIKITQOVGVENLXLTELTTVFGPOITSPALTIQALYN 240
QY 241 LAGNNDYLLTKLGVGNQNLSSGLITGNPILYDSQTLGLGIQVTLPSVGNLNNMRA 300
Db 241 LAGNNDYLLTKLGVGNQNLSSGLITGNPILYDSQTLGLGIQVTLPSVGNLNNMRA 300
QY 301 TYLETLSVSTTKGFASALVPKVMKGVSVIEELDTSCYIEFDLXYCTRIVTFPMSPGIY 360
Db 301 TYLETLSVSTTKGFASALVPKVMKGVSVIEELDTSCYIEFDLXYCTRIVTFPMSPGIY 360
QY 361 SCLSGNTSACMYSTEGALTPPYMTLKGSVIANCKMTTCRCADPPGIIISQNYGEAVSLID 420
Db 361 SCLSGNTSACMYSTEGALTPPYMTLKGSVIANCKMTTCRCADPPGIIISQNYGEAVSLID 420
QY 421 RQSCNVSLDGIITRLSGEFDATYQKNISIQDSQVITVGNLDISTELGNVNNISNALDK 480
Db 421 RQSCNVSLDGIITRLSGEFDATYQKNISIQDSQVITVGNLDISTELGNVNNISNALDK 480
QY 481 LEESNKLKVNKLTSTSTALITYIVLTIVISLVCGILSLVLACLYMYKQKAOQKTLILWG 540
Db 481 LEESNKLKVNKLTSTSTALITYIVLTIVISLVCGILSLVLACLYMYKQKAOQKTLILWG 540
QY 541 NNTLDQMRATTM 553
Db 541 NNTLDQMRATTM 553

RESULT 6

H46329
cell fusion glycoprotein precursor - Newcastle disease virus
N:Contains: fusion glycoprotein F1; fusion glycoprotein F2
C:Species: Newcastle disease virus
C>Date: 31-Dec-1993 #sequence_revision 22-Oct-1999 #text_change 22-Oct-1999
C:Accession: S07422; H46329
R:McGinnes, L.W.; Morrison, T.G.
Virus Res. 5, 343-356, 1986
A:Title: Nucleotide sequence of the gene encoding the Newcastle disease virus fusion protein
A:Reference number: S07422; MUID:87044526; PMID:3776349
A:Accession: S07422
A:Molecule type: mRNA
A:Residues: 1-553 <MCG>
A:Cross-references: EMBL:M21881
A:Experimental source: strain Australia-Victoria
R:Toyoda, T.; Sakaguchi, T.; Hirota, H.; Gotoh, B.; Kuma, K.; Miyata, T.; Nagai, Y.
Virology 169, 273-282, 1989
A:Title: Newcastle disease virus evolution. II. Lack of gene recombination in generating
A:Reference number: A46329; MUID:89204898; PMID:2705298
A:Accession: H46329
A:Molecule type: genomic RNA
A:Residues: 1-65, 'H', 67-553 <TOY>
A:Cross-references: GB:M24700; NID:g293933; PIDN:AAA46650.1; PID:g293934
A:Experimental source: strain AUS/32
C:Genetics:
A:Gene: F
C:Superfamily: parainfluenza virus cell fusion protein
C:Keywords: Glycoprotein; membrane fusion; transmembrane protein
F#1-25/Domain: signal sequence #status predicted <SIG>
F#25-116/Product: cell fusion glycoprotein F2 #status predicted <FF2>
F#112-116/Region: cleavage processing #status predicted
F#117-553/Product: cell fusion glycoprotein F1 #status experimental <FP1>
F#499-526/Domain: transmembrane #status predicted <TM>
F#85,191,366,447,471/Binding site: carbohydrate (Asn) (covalent) #status predicted
F#85,191,366,447,471/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 95.2%; Score 2625; DB 1; Length 553;
Best Local Similarity 95.5%; Pred. No. 2,2e-156;
Matches 528; Conservative 6; Mismatches 19; Indels 0; Gaps 0;

Qy	1	MGSRSSRIPIVPLMLTVRVALALSCVPTSSLDGRPLAAAGIVVTGDKAVNIYTSQTGS	60
Db	1	MGPRSSRIPIPLMTIRIALALSCVHLASLDGRPLAAAGIVVTGDKAVNIYTSQTGS	60
Qy	61	IIIVKLLPNMPKDEACAKAPLEAVNRTLITLLTPGLDSIRRIQESVTTSGGKQGRIGA	120
Db	61	IIIVKLLPNMPKDEACAKAPLEAVNRTLITLLTPGLDSIRRIQESVTTSGRQKRFIGA	120
Qy	121	IIIGAAIGVATAAQITTAASALIQANNAAILRLKERIATNEAVHEVTDGLSQLAVAG	180
Db	121	IIIGSVALGVATAAQITTAASALIQANNAAILRLKESITATIEAVHEVTDGLSQLAVAG	180
Qy	181	KMQQFVNDQFNKTAQELDCIKITQQVGVELNLYITELTTFVFGQITSPALTTIQAALYN	240
Db	181	KMQQFVNDQFNNTAQELDCIKITQQVGVELNLYITELTTFVFGQITSPALTTIQAALYN	240
Qy	241	LAGNMPLYLTIKLGVGNQNLSSLIGSLITGNPILYDSQTQLLGIQVTLPSVGNLNMRA	300
Db	241	LAGNMPLYLTIKLGVGNQNLSSLIGSLITGNPILYDSQTQLLGIQVTLPSVGNLNMRA	300
Qy	301	TYLETLSVSTTKGFASALVPKVMKVGSVIEELDTSYCIETDLIDLYCTRIVTFPMSPGIY	360
Db	301	TYLETLSVSTTKGFASALVPKVMKVGSVIEELDTSYCIETDLIDLYCTRIVTFPMSPGIY	360
Qy	361	SLCSGNTSACMSYKTEGALTTPYMLTKSGSVIANCKMTTCRCADPPGIISQNYGEAVSLID	420
Db	361	SLCNGNTSACMSYKTEGALTTPYMLTKSGSVIANCKMTTCRCADPPGIISQNYGEAVSLID	420
Qy	421	RQSCNVLSDGITTIRLSEGFATYQKNISITQDSQVITVGNLIDSTELGNVNNISINALDK	480
Db	421	RHSCNVLSDGITTIRLSEGFATYQKNISITQDSQVITVGNLIDSTELGNVNNISINALDK	480

Qy 481 LEENSKLDKVNKLTSTSAITYIVLTVISLVCGLISLVACYLWYKQAKOQKTLWMIG 540
 Db 481 LEENSKLDKVNKLTSTSAITYIVLTVISLVCGLISLVACYLWYKQAKOQKTLWMIG 540
 Qy 541 NNTLDQWRATTKM 553
 Db 541 NNTLDQWRATTKM 553

RESULT 7
 D46329
 cell fusion glycoprotein precursor - Newcastle disease virus (strain BI/47)
 N:Contains: fusion glycoprotein F1; fusion glycoprotein F2
 C:Species: Newcastle disease virus
 C:Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 16-Jul-1999
 C:Accession: D46329
 R:Toyoda, T.; Sakaguchi, T.; Hirota, H.; Gotoh, B.; Kuma, K.; Miyata, T.; Nagai,
 Virolgy 169, 273-282, 1989
 A:Title: Newcastle disease virus evolution. II. Lack of gene recombination in
 A:Reference number: A46329; MUID:89204898; PMID:2705298
 A:Accession: D46329
 A:Molecule type: genomic RNA
 A:Residues: 1-553 <TOY>
 A:Cross-References: GB:M24695; NID:G293925; PIDN:AAA46646.1; PID:G293926
 C:Genetics:
 A:Gene: F
 C:Superfamily: parainfluenza virus cell fusion protein
 C:Keywords: Glycoprotein; membrane fusion; transmembrane protein
 F:1-25/Domain: signal sequence #status predicted <SIG>
 F:26-117/Product: cell fusion glycoprotein F2 #status predicted <FF2>
 F:118-553/Product: cell fusion glycoprotein F1 #status predicted <FF1>
 F:495-528/Domain: transmembrane #status predicted <TMN>
 F:85,191,366,447,471/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 95.1%; Score 2622; DB 1; Length 553;
 Best Local Similarity 93.5%; Pred. No. 3.4e-156;
 Matches 517; Conservative 21; Mismatches 15; Indels 0; Gaps 0

Qy 1 MGSSSTRIPVPLMLTVRVALALSCVPTSSLDGRPLAAAGIVTGDKAVNIYTSQTGS 60
 Db 1 MGSRPSTKIPAPMLTIRVALVLSCTCPANSIDGRPLAAAGIVTGDKAVNIYTSQTGS 60
 Qy 61 IIVKLLPNPKDKEACAKAPLEAYNRITLTLLTPLGDSIRRIQESVTTSGGKQGLIGA 120
 Db 61 IIVKLLPNPKDKEACAKAPLDAYNRITLTLLTPLGDSIRRIQESVTTSGGKQGLIGA 120
 Qy 121 IIGGALGVATAAGIITAASALIQAQNAANILRIKERTAAATNEAVHEVTDGLSQLAVAG 180
 Db 121 IIGGALGVATAAGIITAASALIQAQNAANILRIKERTAAATNEAVHEVTDGLSQLAVAG 180
 Qy 181 KMQGFVNDQFNKTAQELDCIKITQQVGVELMLYLTELTTVFPGQITSPALTOITQALYN 240
 Db 181 KMQGFVNDQFNKTAQELDCIKIAQVGVELMLYLTELTTVFPGQITSPALNKLITQALYN 240
 Qy 241 LAGNNDYLLTKLGVGNQVLSLLTGSGLITGNPILYDSQTOLLGIQVTLPSVGNLNNRA 300
 Db 241 LAGNNDYLLTKLIGIGNQVLSLLTGSGLITGNPILYDSQTOLLGIQVTLPSVGNLNNRA 300
 Qy 301 TYLETLVSVTTKGFASALVPKVMKGVSVIELDTSYCIETDLDLYCTRIVTFFMSPGIY 360
 Db 301 TYLETLVSVTTKGFASALVPKVVTVQGSVIELDTSYCIETDLDLYCTRIVTFFMSPGIY 360
 Qy 361 SCLSGNTSACMYSTEGALTTPYMTLKGSVIANKMWTTCRCADPPGIIISQNYGEAVSLID 420
 Db 361 SCLSGNTSACMYSTEGALTTPYMTIKGSVIANKMWTTCRCVNPFGIISQNYGEAVSLID 420
 Qy 421 RQSCNVLSLQGITURLSGEPDATTQKNISIDQSVITGNLIDSTELGNVNNISNALDK 480
 Db 421 RQSCNVLSLGGITURLSGEPDVTQKNISIDQSVITGNLIDSTELGNVNNISNALNK 480
 Qy 481 LEENSKLDKVNKLTSTSAITYIVLTVISLVCGLISLVACYLWYKQAKOQKTLWMIG 540
 Db 481 LEENSKLDKVNKLTSTSAITYIVLTVISLVCGLISLVACYLWYKQAKOQKTLWMIG 540

QY 541 NNTLDMRATTM 553
Db |||||

QY 541 NNTLDMRATTM 553
Db |||||

RESULT 8

VGNZNV

cell fusion glycoprotein precursor - Newcastle disease virus (strain Texas)
N;Contains: fusion glycoprotein F1; fusion glycoprotein F2
C;Species: Newcastle disease virus
C;Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 16-Jul-1999
C;Accession: A34663
R;Taylor, J.; Edbauer, C.; Rey-Senelange, A.; Bouquet, J.F.; Norton, E.; Goebel, S.; De
J. Virol. 64, 1441-1450, 1990
A;Title: Newcastle disease virus fusion protein expressed in a fowlpox virus recombinant
A;Reference number: A34663; MUID:90204652; PMID:2157037
A;Accession: A34663
A;Molecule type: genomic RNA
A;Residues: 1-553 <TAY>
A;Cross-references: EMBL:M33855; MID:g332369; PIDN:AAA46675.1; PID:g332370
C;Genetics:
A;Gene: F
C;Superfamily: parainfluenza virus cell fusion protein
C;Keywords: glycoprotein; membrane fusion; transmembrane protein
F;1-25/Domain: signal sequence #status predicted <SIG>
F;112-116/Region: cleavage processing #status predicted
F;117-553/Product: cell fusion glycoprotein F1 #status predicted <FF1>
F;117-133/Domain: transmembrane #status predicted <TM1>
F;504-521/Domain: transmembrane #status predicted <TM2>
F;85,131,366,447,471,541/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 94.5%; Score 2606; DB 1; Length 553;
Best Local Similarity 94.8%; Pred. No. 3.4e-155;
Matches 524; Conservative 9; Mismatches 20; Indels 0; Gaps 0;

QY 1 MGRSSRTRIPVPLMLTVRVALLSCVPTSSLDGRPLAAGIVTGDKAVNYTSSOTGS 60
Db |||||
QY 1 MGRSSRTRIPVPLMLTVRVALLSCVPTSSLDGRPLAAGIVTGDKAVNYTSSOTGS 60
Db |||||
QY 61 IIVKLLPNMPKDEKACAKAPLEAYNRTLTLLTPLGDSIRRIQESVTTSGGKQRLIGA 120
Db |||||
QY 121 IIGGALGVATAAQITTAASALIQANQANILRLKERIAATNEAVHEVTDGLSOLAVG 180
Db |||||
QY 121 IIGSVALGVATAAQITTAASALIQANQANILRLKESIAATNEAVHEVTDGLSOLAVG 180
QY 181 KMQQFVNDQFNKTAQELDCIKITQOVGVNELNLYLTTLTVPQITSPALTIQALYN 240
Db |||||
QY 181 KMQQFVNDQFNKTAQELDCIKIAQOVGVNELNLYLTTLTVPQITSPALTIQALYN 240
QY 241 LAGNMDYLLTKLGVGNQSSLLIGSLITGNPILYDSQTQLLGIQVTLPSVGNLNMRA 300
Db |||||
QY 241 LAGNMDYLLTKLGVGNQSSLLIGSLITGNPILYDSQTQLLGIQVTLPSVGNLNMRA 300
QY 301 TYLETTSVSTTKGFASALVPKVMKGVSVIEELDTSCIEFDLCTRIIVTFPMSPGIY 360
Db |||||
QY 301 TYLETTSVSTTKGFASALVPKVMKGVSVIEELDTSCIEFDLCTRIIVTFPMSPGIY 360
QY 361 SCLSGNTSACMYKTEGALTTPYMLKGSVIANCKMTTCRCADPPGIIISQNGEAVSLID 420
Db |||||
QY 421 ROSCNVSLDGIITRLSGEFDATYQKNISIQDSQVIVTGNLDISTELGNVNSISNALDK 480
Db |||||
QY 421 RHSCNVSLDGIITRLSGEFDATYQKNISILDSQVIVTGNLDISTELGNVNSISNALNK 480
QY 481 LEENSKLDKVNKLTSTLSALITVILTVISLVGILSLVACHMYKQKQKTLWL 540
Db |||||
QY 481 LEENSKLDKVNKLTSTLSALITVILTVISLVGILSLVACHMYKQKQKTLWL 540

QY 541 NNTLDMRATTM 553
Db |||||

QY 541 NNTLDMRATTM 553
Db |||||

RESULT 9

VGNZNV

cell fusion glycoprotein precursor - Newcastle disease virus (strains Beaudette C and
N;Contains: fusion glycoprotein F1; fusion glycoprotein F2
C;Species: Newcastle disease virus
C;Date: 31-Mar-1988 #sequence_revision 31-Mar-1988 #text_change 16-Jul-1999
C;Accession: A27008; F46329
R;Chambers, P.; Millar, N.S.; Emerson, P.T.
J. Gen. Virol. 67, 2685-2694, 1986
A;Title: Nucleotide sequence of the gene encoding the fusion glycoprotein of Newcastle
A;Reference number: A27008; MUID:87085486; PMID:3025345
A;Accession: A27008
A;Molecule type: mRNA
A;Residues: 1-553 <CHA>
A;Cross-references: GB:X04719; NID:g60933; PIDN:CAA28426.1; PID:g60934
A;Experimental source: strain Beaudette C
R;Toyoda, T.; Sakaguchi, T.; Hirota, H.; Gotoh, B.; Kuma, K.; Miyata, T.; Nagai, Y.
Virology 169, 273-282, 1989
A;Title: Newcastle disease virus evolution. II. Lack of gene recombination in generati
A;Reference number: A46329; MUID:89204898; PMID:2705298
A;Accession: F46329
A;Molecule type: genomic RNA
A;Residues: 1-553 <TOY>
A;Cross-references: GB:M24697; NID:g293929; PIDN:AAA46648.1; PID:g293930
A;Experimental source: strain BEA/45
C;Genetics:
A;Gene: F
C;Superfamily: parainfluenza virus cell fusion protein
C;Keywords: glycoprotein; membrane fusion; transmembrane protein
F;1-25/Domain: signal sequence #status predicted <SIG>
F;26-117/Product: cell fusion glycoprotein F2 #status predicted <FF2>
F;118-553/Product: cell fusion glycoprotein F1 #status predicted <FF1>
F;495-528/Domain: transmembrane #status predicted <TMN>
F;85,131,366,447,471/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 94.4%; Score 2603; DB 1; Length 553;
Best Local Similarity 93.5%; Pred. No. 5.2e-155;
Matches 517; Conservative 19; Mismatches 17; Indels 0; Gaps 0;

QY 1 MGRSSRTRIPVPLMLTVRVALLSCVPTSSLDGRPLAAGIVTGDKAVNYTSSOTGS 60
Db |||||
QY 1 MGRSSRTRIPVPLMLTVRVALLSCVPTSSLDGRPLAAGIVTGDKAVNYTSSOTGS 60
Db |||||
QY 61 IIVKLLPNMPKDEKACAKAPLEAYNRTLTLLTPLGDSIRRIQESVTTSGGKQRLIGA 120
Db |||||
QY 121 IIGGALGVATAAQITTAASALIQANQANILRLKERIAATNEAVHEVTDGLSOLAVG 180
Db |||||
QY 121 IIGSVALGVATAAQITTAASALIQANQANILRLKESIAATNEAVHEVTDGLSOLAVG 180
QY 181 KMQQFVNDQFNKTAQELDCIKITQOVGVNELNLYLTTLTVPQITSPALTIQALYN 240
Db |||||
QY 181 KMQQFVNDQFNKTAQELDCIKIRIAQOVGVNELNLYLTTLTVPQITSPALTIQALYN 240
QY 241 LAGNMDYLLTKLGVGNQSSLLIGSLITGNPILYDSQTQLLGIQVTLPSVGNLNMRA 300
Db |||||
QY 241 LAGNMDYLLTKLGVGNQSSLLIGSLITGNPILYDSQTQLLGIQVTLPSVGNLNMRA 300
QY 301 TYLETTSVSTTKGFASALVPKVMKGVSVIEELDTSCIEFDLCTRIIVTFPMSPGIY 360
Db |||||
QY 301 TYLETTSVSTTKGFASALVPKVMKGVSVIEELDTSCIEFDLCTRIIVTFPMSPGIY 360
QY 361 SCLSGNTSACMYKTEGALTTPYMLKGSVIANCKMTTCRCADPPGIIISQNGEAVSLID 420
Db |||||
QY 361 SCLSGNTSACMYKTEGALTTPYMLKGSVIANCKMTTCRCVNPFGIIISQNGEAVSLID 420
QY 421 ROSCNVSLDGIITRLSGEFDATYQKNISIQDSQVIVTGNLDISTELGNVNSISNALDK 480

Db 421 KSCNVLSLGGITRLSGFDATYQKNSIQDSQVITGNTLSTELGNVNSISNALNK 480
QY 481 LEESNKLKDNVNLKSTGALITYIVLVTVISLVCGILSLVLAACYLAMYKQKQKTLMLG 540
Db 481 LEESNKLKDNVNLKSTGALITYIVLVTVISLVCGILSLVLAACYLAMYKQKQKTLMLG 540
QY 541 NNTLDQMRATTKM 553
Db 541 NNTLDQMRATTKM 553

RESULT 10

S40163
cell fusion protein - Newcastle disease virus
C:Species: Newcastle disease virus
C:Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 24-Nov-1999
C:Accession: S40163
R:Kallman, A.; Zadori, Z.; Kieari, J.; Podor, I.
submitted to the EMBL Data Library, May 1993
A:Description: Nucleotide sequence of the hemagglutinin-neuraminidase (HN) gene of newca
A:Reference number: S40163
A:Accession: S40163
A:Status: preliminary
A:Molecule type: genomic RNA
A:Residues: 1-553 <XAL>
A:Cross-references: EMBL:X71995; NID:G437886; PIDN:CAA50869.1; PID:G437887
C:Superfamily: parainfluenza virus cell fusion protein

Query Match 94.4%; Score 2602; DB 2; Length 553;
Best Local Similarity 94.4%; Pred. No. 6e-155;
Matches 522; Conservative 11; Mismatches 20; Indels 0; Gaps 0;

QY 1 MGRSSTRIPVPLMLTVRVALLSCVCPSTSSLDGRPLAAAGIVTGDKAVNIYTSQTS 60
Db 1 MGRSSTRIPVPLMLIIRALTLSCLRTSSLDGRPLTAAGIVTGDKAVNIYTSQTS 60
QY 61 IIVKLLPNPKDKEACAKAPLEAYNRTLTTLTPLGDSIRRIQESVTTSGGKQRLIGA 120
Db 61 IIVKLLPNPKDKEACAKAPLEAYNRTLTTLTPLGDSIRRIQESVTTSGGKQRLIGA 120
QY 121 IIGGALGVATAAQTAAALIOANONANILRLKERIAATNEAHEVTDGLSOLAVAG 180
Db 121 IIGSVALGVATAAQTAAALIOANONANILRLKESIAATNEAHEVTDGLSOLAVAG 180
QY 181 KMQQFVNDQFNKTAQELDCIKITQQGVVELNLYLTETLVFGPQITSPALTTIQAALYN 240
Db 181 KMQQFVNDQFNNTAQELDCIKITQQGVVELNLYLTETLVFGPQITSPALTTIQAALYN 240
QY 241 LAGGNMYYLLTKLGVGNQSLIGSLITGNPILYDSQTLGLGIVTLPSVGNLNNMRA 300
Db 241 LAGGNMYYLLTKLGVGNQSLIGSLITGNPILYDSQTLGLGIVTLPSVGNLNNMRA 300
QY 301 TYLETLSVSTTKGFASALVPKVMKGVSVIEELDTSYCIETDLVCTRIVTFPMSPGIY 360
Db 301 TYLETLSVSTTKGFASALVPKVMKGVSVIEELDTSYCIETDLVCTRIVTFPMSPGIY 360
QY 361 SCLSGNTSACMSYKTEGALTTPYMTLKGSVIANCKMTTCRCADPPGIISQNYGEAVSLID 420
Db 361 SCLSGNTSACMSYKTEGALTTPYMTLKGSVIANCKMTTCRCADPPGIISQNYGEAVSLID 420
QY 421 RQSCNVLSLGGITRLSGFDATYQKNSIQDSQVITGNTLSTELGNVNSISNALDK 480
Db 421 RQSCNVLSLGGITRLSGFDATYQKNSIQDSQVITGNTLSTELGNVNSISNALDK 480
QY 481 LEESNKLKDNVNLKSTGALITYIVLVTVISLVCGILSLVLAACYLAMYKQKQKTLMLG 540
Db 481 LEESNKLKDNVNLKSTGALITYIVLVTVISLVCGILSLVLAACYLAMYKQKQKTLMLG 540
QY 541 NNTLDQMRATTKM 553
Db 541 NNTLDQMRATTKI 553

RESULT 11

S06345
cell fusion glycoprotein precursor - Newcastle disease virus (strain Italian)
N:Contains: fusion glycoprotein F1; fusion glycoprotein F2
C:Species: Newcastle disease virus
C:Date: 30-Jun-1991 #sequence_revision 30-Jun-1991 #text_change 24-Nov-1999
C:Accession: S06345
R:Espion, D.; de Henau, S.; Letellier, C.; Wemmers, C.D.; Brasseur, R.; Young, J.F.; Gr
Arch. Virol. 95: 79-95, 1987
A:Title: Expression at the cell surface of native fusion protein of the Newcastle dise
A:Reference number: S06345; MUID:87240797; PMID:3592986
A:Accession: S06345
A:Molecule type: genomic RNA
A:Residues: 1-553 <ESP>
A:Cross-references: EMBL:M17710
A:Note: It is uncertain whether Met-1 or Met-14 is the initiator
C:Genetics:
A:Gene: F
C:Superfamily: parainfluenza virus cell fusion protein
C:Keywords: glycoprotein; transmembrane protein
F:1-31/Domain: signal sequence #status predicted <SIG>
F:32-116/Product: fusion glycoprotein F2 #status predicted <F2P>
F:117-553/Product: fusion glycoprotein F1 #status predicted <F1P>
F:495-525/Domain: transmembrane #status predicted <TM>
F:85,191,366,447,471,541/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 94.3%; Score 2599; DB 2; Length 553;
Best Local Similarity 94.4%; Pred. No. 9.2e-155;
Matches 522; Conservative 12; Mismatches 19; Indels 0; Gaps 0;

QY 1 MGRSSTRIPVPLMLTVRVALLSCVCPSTSSLDGRPLAAAGIVTGDKAVNIYTSQTS 60
Db 1 MGRSSTRIPVPLMLIIRALTLSCLRTSSLDGRPLAAAGIVTGDKAVNIYTSQTS 60
QY 61 IIVKLLPNPKDKEACAKAPLEAYNRTLTTLTPLGDSIRRIQESVTTSGGKQRLIGA 120
Db 61 IIVKLLPNPKDKEACAKAPLEAYNRTLTTLTPLGDSIRRIQESVTTSGGKQRLIGA 120
QY 121 IIGGALGVATAAQTAAALIOANONANILRLKERIAATNEAHEVTDGLSOLAVAG 180
Db 121 IIGSVALGVATAAQTAAALIOANONANILRLKESIAATNEAHEVTDGLSOLAVAG 180
QY 181 KMQQFVNDQFNKTAQELDCIKITQQGVVELNLYLTETLVFGPQITSPALTTIQAALYN 240
Db 181 KMQQFVNDQFNNTAQELDCIKITQQGVVELNLYLTETLVFGPQITSPALTTIQAALYN 240
QY 241 LAGGNMYYLLTKLGVGNQSLIGSLITGNPILYDSQTLGLGIVTLPSVGNLNNMRA 300
Db 241 LAGGNMYYLLTKLGVGNQSLIGSLITGNPILYDSQTLGLGIVTLPSVGNLNNMRA 300
QY 301 TYLETLSVSTTKGFASALVPKVMKGVSVIEELDTSYCIETDLVCTRIVTFPMSPGIY 360
Db 301 TYLETLSVSTTKGFASALVPKVMKGVSVIEELDTSYCIETDLVCTRIVTFPMSPGIY 360
QY 361 SCLSGNTSACMSYKTEGALTTPYMTLKGSVIANCKMTTCRCADPPGIISQNYGEAVSLID 420
Db 361 SCLSGNTSACMSYKTEGALTTPYMTLKGSVIANCKMTTCRCADPPGIISQNYGEAVSLID 420
QY 421 RQSCNVLSLGGITRLSGFDATYQKNSIQDSQVITGNTLSTELGNVNSISNALDK 480
Db 421 RQSCNVLSLGGITRLSGFDATYQKNSIQDSQVITGNTLSTELGNVNSISNALDK 480
QY 481 LEESNKLKDNVNLKSTGALITYIVLVTVISLVCGILSLVLAACYLAMYKQKQKTLMLG 540
Db 481 LEESNKLKDNVNLKSTGALITYIVLVTVISLVCGILSLVLAACYLAMYKQKQKTLMLG 540
QY 541 NNTLDQMRATTKM 553
Db 541 NNTLDQMRATTKI 553

RESULT 12

A36830
cell fusion glycoprotein precursor - Newcastle disease virus (strain HER/33)
N/Contains: fusion glycoprotein F1; fusion glycoprotein F2
C/Species: Newcastle disease virus
C/Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 16-Jul-1999
C/Accession: A36830
R/Toyoda, T.; Sakaguchi, T.; Hirota, H.; Gotch, B.; Kuma, K.; Miyata, T.; Nagai, Y.
Virology 169, 273-282, 1989
A/Title: Newcastle disease virus evolution. II. Lack of gene recombination in generating
A/Reference number: A46329; MUID:99204898; PMID:2705298
A/Accession: A36830
A/Molecule type: Genomic RNA
A:Residues: 1-553 <TCY>
A:Cross-references: GB:M24702; NID:G293937; PIDN:AAA46652.1; PID:G293938
C/Genetics:
A:Gene: F
C;Superfamily: parainfluenza virus cell fusion protein
C;Keywords: glycoprotein; membrane fusion; transmembrane protein
F;1-25/Domain: signal sequence #status predicted <SIG>
F;26-117/Product: cell fusion glycoprotein F1 #status predicted <FF2>
F;118-553/Product: cell fusion glycoprotein F2 #status predicted <FF1>
F;495-528/Domain: transmembrane #status predicted <TM>
F;85,191,366,447,471/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 94.2%; Score 2598; DB 1; Length 553;
Best Local Similarity 94.4%; Pred. No. 1.1e-154;
Matches 522; Conservative 11; Mismatches 20; Indels 0; Gaps 0;

Qy 1 MGRSSRIPIVPLMLTVRVALALSCVPTSSLDGRPLAAAGIVTGDKAVNIYTSSTGTS 60
Db 1 MGRSSRIPIVPPMLIRIIVLTISCILTSLDGRPLAAAGIVTGDKAVNIYTSSTGTS 60
Qy 61 IIVKLLPNMPKDEACAKAPLEAVNRILTLLTPLGDSIRRIQESVTTSGGKQRLIGA 120
Db 61 IIVKLLPNMPKDEACAKAPLEAVNRILTLLTPLGDSIRRKQESVTTSGRRQRRIGA 120
Qy 121 IIGGALGVATAAGIITAASALIQANQAANILRLKERIATNEAVHEVTDGLSQAIVAG 180
Db 121 IIGSVALGVATAAGIITAASALIQANQAANILRLKESIAATNEAVHEVTDGLSQAIVAG 180
Qy 181 KMQQFVNDQFNKTAQELDCIKITQQGVVELNLYLTETTTVFGPOITSPALTIQALYN 240
Db 181 KMQQFVNDQFNNTAQELDCIKITQQGVVELNLYLTETTTVFGPOITSPALTIQALYN 240
Qy 241 LAGNMDYLLTKLGVGNQSLGSLGITGNPLYDSQTOLLGIQVTLPSVGNLNNRA 300
Db 241 LAGNMDYLLTKLGVGNQSLGSLGITGNPLYDSQTOLLGIQVTLPSVGNLNNRA 300
Qy 301 TYLETLSVTTKGFASALVPKVMKGVSVIEELDTSYCIETDLDLYCTRIVTFPMSPGIY 360
Db 301 TYLETLSVTTKGFASALVPKVTQVGSVIEELDTSYCIETDLDLYCTRIVTFPMSPGIY 360
Qy 361 SCLSGNTSACMYSTEGEALTTPYMLTKGSVIANCKMTTCRCADPPGIISQNYGEAVSLID 420
Db 361 SCLSGNTSACMYSTEGEALTTPYMLTKGSVIANCKMTTCRCADPPGIISQNYGEAVSLID 420
Qy 421 RQSCNVLSLDGITLRLSGEPATYQKNISIODSQVITGNLDISTELGNVNNISINLADK 480
Db 421 RHCNVLSLDGITLRLSGEPATYQKNISILDQSVITGNLDISTELGNVNNISINLANK 480
Qy 481 LEENSCLDKVNVKLTSTSAITYITLTVISLVGILSLVLACYLIMYKQAQKTLWLIG 540
Db 481 LEENSCLDKVNVRLTSTSAITYITLTVISLVGILSLVLACYLIMYKQAQKTLWLIG 540
Qy 541 NNTLDQMRATTYK 553
Db 541 NNTLDQMRATTXI 553

RESULT 13
G46329
cell fusion glycoprotein precursor - Newcastle disease virus (strain TEX/48)
N/Contains: fusion glycoprotein F1; fusion glycoprotein F2

C:Species: Newcastle disease virus
C>Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 16-Jul-1999
C:Accession: G46329; S11266
R:Toyoda, T.; Sakaguchi, T.; Hirota, H.; Gotch, B.; Kuma, K.; Miyata, T.; Negai, Y.
Virology 169, 273-282, 1989
A:Title: Newcastle disease virus evolution. II. Lack of gene recombination in generation II.
A:Reference number: A46329; MUID:89204898; PMID:2705298
A:Accession: G46329
A:Molecule type: Genomic RNA
A:Residues: 1-553 <TOY>
A:Cross-references: GB:M24698; NID:G293931; PIDN:AAA46649.1; PID:G293932
R:Richardson, C.D.; Scheid, A.; Choppin, P.W.
Virology 105, 205-222, 1980
A:Title: Specific inhibition of paramyxovirus and myxovirus replication by oligopeptidase A.
A:Reference number: S11266; MUID:81016739; PMID:7414950
A:Molecule type: S11266
A:Molecule type: protein
A:Residues: 117-136 <RIC>
C:Genetics:
A:Gene: F
C:Superfamily: parainfluenza virus cell fusion protein
C:Keywords: Glycoprotein; membrane fusion; transmembrane protein
F:1-25/Domain: signal sequence #status predicted <SIG>
F:26-117/Product: cell fusion glycoprotein F2 #status predicted <PF2>
F:118-553/Product: cell fusion glycoprotein F1 #status predicted <FF1>
F:495-528/Domain: transmembrane #status predicted <TMN>
F:85,191,366,447,471/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 94.1%; Score 2593; DB 1; Length 553;
Best Local Similarity 93.1%; Pred. No. 2.2e-154;
Matches 515; Conservative 19; Mismatches 19; Indels 0; Gaps 0;

Qy 1 MGRSSRTIPVPLMLTVRVALALSCVPTSSDGRPLAAAGIVTGDKAVNIYTSQTGS 60
Db 1 MGPRPSTKNPTFPMMLTVRVALVSLICPANSIDGRPLAAAGIVTGDKAVNIYTSQTGS 60

Qy 61 IIVKLLPNMPKDEACAKAPLEAVNRTLTLLTPLGDSIRRIQESVTTSGGKGQLIGA 120
Db 61 IIVKLLPNLPKDEACAKAPLDVNRLLTLLTPLGDSIRRIQESVTTSGRRQRFIGA 120

Qy 121 IIGGAALGVATAAOITTAASALIQAONANAANILRLKRIATNEAVEHVTDLGSLQAVVG 180
Db 121 IIGGVALGVATAQITTAARALIQAONANAANILRLKESIAATNEAVEHVTDLGSLQAVVG 180

Qy 181 KMOQFVNDQFNKTAQELDCIKITQOVGVNELNLYLTELTVFGPQITSPALTOIQAALYN 240
Db 181 KMQQFVNDQFNKTAQESGIRIAQOVGVNELNLYLTELTVFGPQITSPALNKLTIOALYN 240

Qy 241 LAGGNMVDLLTKLGVNNQLSLIGSLITGNPILYDSQTLLGIQVTLPSVGNLNNMRA 300
Db 241 LAGGNMVDLLTKLGVNNQLSLIGSLITGNPILYDSQTLLGIQVTLPSVGNLNNMRA 300

Qy 301 TYLETLVSSTTKGFASALVPKVMKGVSVIEBELDTSYCIETDLDLCTYTRIVTFPMSPGIY 360
Db 301 TYLETLVSSTTRGFASALVPKVVTVQGVSVIEBELDTSYCIETDLDLCTYTRIVTFPMSPGIY 360

Qy 361 SCLSGNTSACMYKTEGALTTPYMTLKGSVIANCKMTTCRCADPGIISQNTYGEAVSLID 420
Db 361 SCLSGNTSACMYKTEGALTTPYMTIKGSVIANCKMTTCRCVNPPIGISQNTYGEAVSLID 420

Qy 421 QSCNVLSLDGLTLRLSEGFATYQKNLSIQDSQVITGNLIDISTELGNVNNISINALDK 480
Db 421 QSCNVLSLDGLTLRLSEGFATYQKNLSIQDSQVITGNLIDISTELGNVNNISINALNK 480

Qy 481 LEENSKLDKVNVKLTSTTSALITYIVLTIVISLVCGILSLVLCYLMYKKAQOKTLLWLIG 540
Db 481 LEENSKLDKVNVKLTSTTSALITYIVLTIVISLVFGILSLVLCYLMYKKAQOKTLLWLIG 540

Qy 541 NNTLDDQMRATTM 553
Db 541 NNTLDDQMRATTM 553

RESULT 13
G46329
cell fusion glycoprotein precursor - Newcastle disease virus (strain TEX/48)
N:Contains: fusion glycoprotein F1; fusion glycoprotein F2

RESULT 14

B36830
cell fusion glycoprotein precursor - Newcastle disease virus (strain ITA/45)
N/Contains: fusion glycoprotein F1; fusion glycoprotein F2
C/Species: Newcastle disease virus
C/Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 07-May-1999
C/Accession: B36830
R/Schaper, U.M.; Fuller, F.J.; Ward, M.D.W.; Mehrotra, Y.; Stone, H.O.; Stripp, B.R.;
Virolgy 165, 291-295, 1988
A/Title: Nucleotide sequence of the envelope protein genes of a highly virulent, neuro-
virulent Newcastle disease virus evolution. II. Lack of gene recombination in generating
A/Reference number: A46329; MUID:89204898; PMID:2705298
A/Accession: B36830
A/Molecule type: genomic RNA
A/Residues: 1-553 <TOY>
A/Cross-references: GB:M24703
C/Genetics:
A/Gene: F
C/Superfamily: parainfluenza virus cell fusion protein
C/Keywords: glycoprotein; membrane fusion; transmembrane protein
F1-25/Domain: signal sequence #status predicted <SIG>
F26-117/Product: cell fusion glycoprotein F2 #status predicted <FP2>
F118-553/Product: cell fusion glycoprotein F1 #status predicted <FP1>
F495-528/Domain: transmembrane #status predicted <TMN>
F/85,191,366,447,471/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 94.0%; Score 2592; DB 1; Length 553;
Best Local Similarity 94.2%; Pred. No. 2.5e-154;
Matches 521; Conservative 12; Mismatches 20; Indels 0; Gaps 0;

QY	1	MGRSSTRIPVPLMLTVRVALALSCVCPPTSSLDGRPLAAGIVVTGDKAVNIYTSSQTGS	60
DB	1	MGRSSTRIPVPLMLTVRVALALSCVCPPTSSLDGRPLAAGIVVTGDKAVNIYTSSQTGS	60
QY	61	IIVKLLPNMPKDEKACAPLEAYNRTLTLLTPLGDSIRRIQESVTTSGGKQGRIGLA	120
DB	61	IIVKLLPNMPKDEKACAPLEAYNRTLTLLTPLGDSIRRIQESVTTSGGKQGRIFGA	120
QY	121	IIGGAALGVATAAQITAAALIQANONANILRLKERIAATNEAVHEVTDGLSQLAVAG	180
DB	121	IIGSVALGVATAAQITAAALIQANONANILRLKESIAATNEAVHEVTDGLSQLAVAG	180
QY	181	KMQQFVNDQFNKTAQELDCIKITQGVGVELNLYLTETTVFGPQITSPALTIQALYN	240
DB	181	KMQQFVNDQFNKTAQELDCIKITQGVGVELNLYLTETTVFGPQITSPALTIQALYN	240
QY	241	LAGGNMDYLLTKLGVGNQLSSGLITGNPILYDSQTLLGIQVTLPSVGNLNNMRA	300
DB	241	LAGGNMDYLLTKLGVGNQLSSGLITGNPILYDSQTLLGIQVTLPSVGNLNNMRA	300
QY	301	TYLETLSVSTTKGFASALVPKVMKGVSVIEBLDTSYCIETDLTYCTRIVTFPMSPGIY	360
DB	301	TYLETLSVSTTKGFASALVPKVMKGVSVIEBLDTSYCIETDLTYCTRIVTFPMSPGIY	360
QY	361	SCLSGNTSACMSKTEGALTTPYMTLKGSVIANCKMTTCRCADPPGIISQNGEAVSLID	420
DB	361	SCLSGNTSACMSKTEGALTTPYMTLKGSVIANCKMTTCRCADPPGIISQNGEAVSLID	420
QY	421	RQSCNVSLDGTITLRLSGEFDATYQKNISIQDSQVIVTGNLIDISTELGNVNNISNALDK	480
DB	421	RHSCNVSLDGTITLRLSGEFDATYQKNISILDSQVIVTGNLIDISTELGNVNNISNALNK	480
QY	481	LEESNKLDKNNVKTSTTSALITYVLTVISVAVCGILSVLACILMYKQAKOQKTLMLG	540
DB	481	LEESNKLDKNNVKTSTTSALITYVLTVISVAVCGILSVLACILMYKQAKOQKTLMLG	540
QY	541	NTTLDQMRATTQK 553	
DB	541	NTTLDQMRATTKI 553	

RESULT 15

VGNZGB
cell fusion glycoprotein precursor - Newcastle disease virus (strain Texas G.B.)

N/Contains: fusion glycoprotein F1; fusion glycoprotein F2
C/Species: Newcastle disease virus
C/Date: 31-Dec-1989 #sequence_revision 31-Dec-1989 #text_change 25-Oct-1996
C/Accession: B29201
R/Schaper, U.M.; Fuller, F.J.; Ward, M.D.W.; Mehrotra, Y.; Stone, H.O.; Stripp, B.R.;
Virolgy 165, 291-295, 1988
A/Title: Nucleotide sequence of the envelope protein genes of a highly virulent, neuro-
virulent Newcastle disease virus evolution. II. Lack of gene recombination in generating
A/Reference number: A94379; MUID:88265873; PMID:3388773
A/Accession: B29201
A/Molecule type: mRNA
A/Residues: 1-553 <SCH>
A/Experimental source: strain Texas G.B.
C/Genetics:
A/Gene: F
C/Superfamily: parainfluenza virus cell fusion protein
C/Keywords: glycoprotein; membrane fusion; transmembrane protein
F1-31/Domain: signal sequence #status predicted <SIG>
F32-111/Product: cell fusion glycoprotein F2 #status predicted <FP2>
F112-116/Region: cleavage processing #status predicted
F/117-553/Product: cell fusion glycoprotein F1 #status predicted <FP1>
F/9,85,191,366,447,471/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 93.9%; Score 2589; DB 1; Length 553;
Best Local Similarity 92.9%; Pred. No. 3.9e-154;
Matches 514; Conservative 19; Mismatches 20; Indels 0; Gaps 0;

QY	1	MGRSSTRIPVPLMLTVRVALALSCVCPPTSSLDGRPLAAGIVVTGDKAVNIYTSSQTGS	60
DB	1	MGRSSTRIPVPLMLTVRVALALSCVCPPTSSLDGRPLAAGIVVTGDKAVNIYTSSQTGS	60
QY	61	IIVKLLPNMPKDEKACAPLEAYNRTLTLLTPLGDSIRRIQESVTTSGGKQGRIGLA	120
DB	61	IIVKLLPNMPKDEKACAPLEAYNRTLTLLTPLGDSIRRIQESVTTSGGKQGRIFGA	120
QY	121	IIGGAALGVATAAQITAAALIQANONANILRLKERIAATNEAVHEVTDGLSQLAVAG	180
DB	121	IIGGVALGVATAAQITAAALIQANONANILRLKESIAATNEAVHEVTDGLSQLAVAG	180
QY	181	KMQQFVNDQFNKTAQELDCIKITQGVGVELNLYLTETTVFGPQITSPALTIQALYN	240
DB	181	KMQQFVNDQFNKTAQELDCIKITQGVGVELNLYLTETTVFGPQITSPALTIQALYN	240
QY	241	LAGGNMDYLLTKLGVGNQLSSGLITGNPILYDSQTLLGIQVTLPSVGNLNNMRA	300
DB	241	LAGGNMDYLLTKLGVGNQLSSGLITGNPILYDSQTLLGIQVTLPSVGNLNNMRA	300
QY	301	TYLETLSVSTTKGFASALVPKVMKGVSVIEBLDTSYCIETDLTYCTRIVTFPMSPGIY	360
DB	301	TYLETLSVSTTKGFASALVPKVMKGVSVIEBLDTSYCIETDLTYCTRIVTFPMSPGIY	360
QY	361	SCLSGNTSACMSKTEGALTTPYMTLKGSVIANCKMTTCRCADPPGIISQNGEAVSLID	420
DB	361	SCLSGNTSACMSKTEGALTTPYMTLKGSVIANCKMTTCRCADPPGIISQNGEAVSLID	420
QY	421	RQSCNVSLDGTITLRLSGEFDATYQKNISIQDSQVIVTGNLIDISTELGNVNNISNALDK	480
DB	421	RQSCNVSLDGTITLRLSGEFDATYQKNISIQDSQVIVTGNLIDISTELGNVNNISNALNK	480
QY	481	LEESNKLDKNNVKTSTTSALITYVLTVISVAVCGILSVLACILMYKQAKOQKTLMLG	540
DB	481	LEESNKLDKNNVKTSTTSALITYVLTVISVAVCGILSVLACILMYKQAKOQKTLMLG	540
QY	541	NTTLDQMRATTQK 553	
DB	541	NTTLDQMRATTKM 553	

Search completed: April 18, 2004, 02:33:33
Job time : 48 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: April 17, 2004, 06:54:07 ; Search time 97 Seconds
(without alignments)
1610.812 Million cell updates/sec

Title: US-10-725-841-2

Perfect score: 2757
Sequence: 1 MGRSSTRIPVPLMLTVRVA.....XTLLWLGNNLTQMRATTKM 553

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_29Jan04.*
1: Geneseq1980s.*
2: Geneseq1990s.*
3: Geneseq2000s.*
4: Geneseq2001s.*
5: Geneseq2002s.*
6: Geneseq2003as.*
7: Geneseq2003bs.*
8: Geneseq2004s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	2724	98.8	553	2 AAR10065	Aar10065 Newcastle
2	2716	98.5	553	6 ABR56236	ABR56236 Newcastle
3	2620	95.0	1103	6 ABR39678	ABR39678 Amino aci
4	2616	94.9	553	3 AAY51231	Aay51231 Newcastle
5	2610	94.7	553	2 AAR58858	Aar58858 Newcastle
6	2610	94.7	553	2 AAR49141	Aar49141 Newcastle
7	2610	94.7	553	2 AAW06828	Aaw06828 Newcastle
8	2610	94.7	553	2 AAW10691	Aaw10691 Newcastle
9	2610	94.7	553	2 AAY21983	Aay21983 Seq ID No
10	2610	94.7	553	3 AAY58183	Aay58183 NDV fusio
11	2610	94.7	553	3 AAB36039	Aab36039 Protein e
12	2606	94.5	553	2 AAR14480	Aar14480 Newcastle
13	2606	94.5	553	2 AAR44941	Aar44941 Newcastle
14	2603	94.4	553	1 AAP70176	Aap70176 Sequence
15	2493.5	90.4	564	5 ABG31709	ABg31709 Newcastle
16	2401	87.1	526	1 AAP80986	Aap80986 Sequence
17	2386	86.5	526	2 AAR20501	Aar20501 Newcastle
18	2086.5	75.7	436	6 ABO10250	ABO10250 Newcastle
19	2065	74.9	437	4 AAU14030	Aau14030 Peptide s
20	717	26.0	529	6 ABJ18515	ABj18515 Human Cry
21	715	25.9	529	6 ABJ18516	ABj18516 Canine pa
22	714	25.9	551	6 ABJ18506	ABj18506 Human Cry
23	712	25.8	551	6 ABJ18514	ABj18514 Simian vi
24	707	25.6	551	6 ABJ18513	ABj18513 Simian vi
25	706	25.6	529	4 ABP98712	ABp98712 Canine pa

26	696.5	25.3	532	6 ABJ18507	ABj18507 Human Cry
27	694.5	25.2	538	4 AAB67476	Aab67476 Amino aci
28	689	25.0	542	2 AAR24076	Aar24076 Para-infl
29	623.5	22.6	662	2 AAR83304	Aar83304 Canine di
30	623.5	22.6	662	5 AAM47653	Aam47653 Canine di
31	621.5	22.5	662	3 AAB08102	Aab08102 Amino aci
32	621.5	22.5	662	4 AAM50124	Aam50124 Canine di
33	610.5	22.1	550	2 AAR42394	Aar42394 Moraten h
34	610.5	22.1	550	4 AAB73722	Aab73722 Measles v
35	608.5	22.1	550	2 AAR34540	Aar34540 F protein
36	606.5	22.0	550	2 AAR42396	Aar42396 Chicago 1
37	606.5	22.0	550	2 AAR42397	Aar42397 Consensus
38	606.5	22.0	550	2 AAR42395	Aar42395 San Diego
39	605.5	22.0	550	2 AAW94759	Aaw94759 Mutant me
40	605.5	22.0	550	4 AAB73721	Aab73721 Measles v
41	602.5	21.9	550	2 AAW94760	Aaw94760 Mutant me
42	590.5	21.4	449	6 ABJ18509	ABj18509 Human Cry
43	552	20.0	539	2 AAR39283	Aar39283 Parainflu
44	534	19.4	438	6 ABO10249	ABO10249 Canine di
45	522.5	19.0	439	4 AAU14029	Aau14029 Peptide s

ALIGNMENTS

RESULT 1
AAR10065
ID AAR10065 standard; protein; 553 AA.
XX
AC AAR10065;
XX
DT 25-MAR-2003 (revised)
DT 14-MAR-1991 (first entry)
XX
DE Newcastle disease virus (NDV) F gene product.
XX
KW Avipoxvirus; fowlpoxvirus; vaccine.
XX
OS Newcastle disease virus.
XX
PN EP404576-A.
XX
PD 27-DEC-1990.
XX
PF 21-JUN-1990; 90EP-00306806.
XX
PR 22-JUN-1989; 89JP-00160157.
XX
PA (JAPG) NIPPON ZEON KK.
PA (SHIO) SHIONOGI & CO LTD.
XX (YANA /) YANAGIDA N.
XX Yangida N, Saeki S, Okawa S, Knamogawa K, Iritani Y, Sawaguchi K;
XX WPI: 1991-001591/01.
XX N-PSDB; AALQ10060.
XX
PT Recombinant avipox virus - contg. CDNA coding for Newcastle disease virus
in region non-essential for proliferation, used as live vaccine in fowls.
XX
PS Claim 3; Fig 3; 23pp; English.
XX
CC The sequence encoding the protein may be incorporated into a recombinant
CC Avipoxvirus and used as a live vaccine in fowls, providing immunity to
CC fowlpoxvirus and NDV. (Updated on 25-MAR-2003 to correct PA field.)
XX
SQ Sequence 553 AA;

Query Match 98.8%; Score 2724; DB 2; Length 553;
Best Local Similarity 98.4%; Pred. No. 9.8e-226;
Matches 544; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

QY 1 MGRSSTRIPVPLMLTVRVALSCVFTSSLDGRPLAAAGIVVTGDKAVNIYTSQTGS 60

Db	1	MGSRSTRIPVPMULTVIMTALSVCPTSSLDGRPLAAAGIVVTGDKAVNIYTSQTGS	60
Qy	61	IIIVKLLPNMPKDEKACAPLEAYNRTLTTLLTPLGDSIRRIQESVTTTSGGKGQRLIGA	120
Db	61	IIIVKLLPNMPKDEKACAPLEAYNRTLTTLLTPLGDSIRRIQESVTTTSGGKGQRLIGA	120
Qy	121	IIGGAALGVATAAQITTAASALIQAONQANAIIIRLKERIAATNEAVEHEVTDGLSQLAVAG	180
Db	121	IIGGVALGVATAAQITTAASALIQAONQANAIIIRLKERIAATNEAVEHEVTDGLSQLAVAG	180
Qy	181	KMQQFVNDQFNKTAQELDCIKITQOVGVNELNYLTELTTVPGPQITSPALTOITQALYN	240
Db	181	KMQQFVNDQFNKTAQELDCIKITQOVGVNELNYLTELTTVPGPQITSPALTOITQALYN	240
Qy	241	LAGGNMVDYLLTKLGVGNQOLSSLIGSLITGNPILLYDSQTLGLIGQVTLPSVGNLNNMRA	300
Db	241	LAGGNMVDYLLTKLGVGNQOLSSLIGSLITGNPILLYDSQTLGLIGQVTLPSVGNLNNMRA	300
Qy	301	TYLETLSVSTTKGFASALVPKVMKVGVIEBELDTSYCIETDLDLXYCTRIVTFPMPSPGIY	360
Db	301	TYLETLSVSTTKGFASALVPKVMKVGVIEBELDTSYCIETDLDLXYCTRIVTFPMPSPGIY	360
Qy	361	SCLSGNTSACMYSKTEGALTTPYMTLKGSVIANCKMTTCRCADPPGIIISONTGEAVSLID	420
Db	361	SCLSGNTSACMYSKTEGALTTPYMTLKGSVIANCKMTTCRCADPPGIIISONTGEAVSLID	420
Qy	421	RQSCNVLSLDGTLRLSGEPDATYQKNISIQDSQVIVTGNLIDISTELGNVNNSISNALDK	480
Db	421	RQSCNVLSLDGTLRLSGEPDATYQKNISIQDSQVIVTGNLIDISTELGNVNNSISNALDK	480
Qy	481	LEESNSKLDKVNVLKLTSTTSALITYTLVTIVISLVCGLSILVLACYLMYKQAKQKTLIWLIG	540
Db	481	LEESNSKLDKVNVLKLTSTTSALITYTLVTIVISLVCGLSILVLACYLMYKQAKQKTLIWLIG	540
Qy	541	NNTLIDQMRATTKM	553
Db	541	NNTLIDQMRATTKM	553

RESULT 2
ABR56236
ID ABR56236 standard; protein; 553 AA.

Identifying, screening or modifying anti-viral agents, by generating a 3-dimensional structure model of respiratory Syncytial virus-F protein having a target site to interact with an anti-viral agent that inhibit RSV-F.

The present invention relates to a method (M1) for identifying a candidate anti-viral agent (I), screening compounds and/or chemical complexes for (I), modifying (I) to improve anti-viral activity, or producing anti-viral agents by generating a 3-dimensional structure model of Respiratory Syncytial Virus (RSV) Fusion (F)-protein with 3-dimensional structure of target site to which an anti-viral agent may interact and thus inhibit RSV-F protein activity. The present sequence is the Newcastle Disease Virus (NDV) F-protein used in a sequence alignment with the RSV F-protein sequence (ABR56234)

Sequence 553 AA;

RESULT 3
ABR39678
ID ABR39678 standard; protein; 1103 AA.
XX
XX ABR39678;
XX
DT 23-JUN-2003 (first entry)

RESULT 3
APPENDIX 79


```
PN US9525358-A.
XX 20-JUL-1999.
XX PF 07-JUN-1995; 95US-00484575.
XX PR 26-FEB-1993; 93US-00024156.
XX PR 28-FEB-1994; 94WO-US002252.
XX PA (SYTR ) SYNTRO CORP.
XX PI Junker DE, Cochran MD;
XX DR WPI; 1999-418249/35.
XX DR N-PSDB; AAX81147.
XX
XX Fowlpox viruses, useful as vaccines for immunization of chickens/turkeys
XX against Fowlpox and Newcastle disease virus.
XX
XX PS Disclosure; Col 61-70; 108pp; English.
XX
XX CC The invention relates to a recombinant fowlpox virus (FPV) comprising a
XX foreign DNA inserted into a region of the fowlpox virus genome
XX corresponding to a 2.8 kb EcoRI fragment, capable of being expressed in a
XX host cell. The virus is used as a vaccine for immunising chickens against
XX Newcastle disease virus (NDV), Fowlpox, and infectious Laryngotracheitis
XX
XX SQ Sequence 553 AA;
Query Match 94.7%; Score 2610; DB 2; Length 553;
Best Local Similarity 93.1%; Pred. No. 6.7e-216;
Matches 515; Conservative 21; Mismatches 17; Indels 0; Gaps 0;
QY 1 MGSRSSTPIPVMLTIVRVALSCVPTSSLDGRPLAAGIVVTCGKAVNIYTSQTGS 60
Db 1 MGSRETNKPNMPTIRVALVSLCIPANSIDGRPLAAGIVVTCGKAVNIYTSQTGS 60
QY 61 IIVKLLPNPKDKEACAKAPLEAYNRTLTLLTPLGDSIRRIQESVTTSGGKQGRLLGA 120
Db 61 IIVKLLPNPKDKEACAKAPLEAYNRTLTLLTPLGDSIRRIQESVTTSGGKQGRLLGA 120
QY 121 IIGGVALGVATAAQITAAALIQAKQNAANILRLKESIAATNEAVHEVTDGLSOLAVAVG 180
Db 121 IIGGVALGVATAAQITAAALIQAKQNAANILRLKESIAATNEAVHEVTDGLSOLAVAVG 180
QY 181 KMQQFVNDQFNKTAQELDCIKITQQVGVNELNYLTETTVFGPQITSPALTOITQALYN 240
Db 181 KMQQFVNDQFNKTAQELDCIKITQQVGVNELNYLTETTVFGPQITSPALTOITQALYN 240
QY 241 LAGGNDYLLTKLGVGNQSLIGSLITGNPILYDSOTQLLGIQVITLPSVGNLNNMRA 300
Db 241 LAGGNDYLLTKLGVGNQSLIGSLITGNPILYDSOTQLLGIQVITLPSVGNLNNMRA 300
QY 301 TYLETLVSSTTKGFASALVPKVMKGVSVIEELDTSCYIETDLDTCTRTVTFPMSPGIY 360
Db 301 TYLETLVSSTTKGFASALVPKVMKGVSVIEELDTSCYIETDLDTCTRTVTFPMSPGIY 360
QY 361 SCLSGNTSACMYSKTEGALTTPMTVLKGSVIANCKMTTCRCADPPGIIISQNYGEAVSLID 420
Db 361 SCLSGNTSACMYSKTEGALTTPMTVLKGSVIANCKMTTCRCVNPPIISQNYGEAVSLID 420
QY 421 QSCNVLSLDGITRLSGSEFDATYQKNISIQDSQVITVGNLNDISTELGNVNSISNALDK 480
Db 421 QSCNVLSLDGITRLSGSEFDATYQKNISIQDSQVITVGNLNDISTELGNVNSISNALDK 480
QY 481 LEESNKLKVNKLTSTSLIITVIVLTVISLVCGLISLVLACVLMYKQAKQKTLILWG 540
Db 481 LEESNKLKVNKLTSTSLIITVIVLTVISLVCGLISLVLACVLMYKQAKQKTLILWG 540
QY 541 NNTLDQWRATTM 553
Db 541 NNTLDQWRATTM 553
```

RESULT 10

```
RAY58183
ID AAY58183 standard; protein; 553 AA.
XX AAY58183;
XX 14-MAR-2000 (first entry)
XX NDV fusion (F) protein.
XX
XX Fowlpox virus; FPV; recombinant; antigenic protein; expression;
XX infectious laryngotracheitis virus; ILTV; Newcastle disease virus; NDV;
XX Marek's disease virus; cytokerin; promoter; homologous recombination;
XX homology vector; multivalent; live vaccine; fusion protein.
XX
XX OS Newcastle disease virus.
XX
XX FH Key Location/Qualifiers
XX Domain 501..527
XX /note= "Transmembrane anchor domain"
XX
XX US6001369-A.
XX 14-DEC-1999.
XX 07-JUN-1995; 95US-00477459.
XX 26-FEB-1993; 93US-00024156.
XX 28-FEB-1994; 94WO-US002252.
XX (SYTR ) SYNTRO CORP.
XX Junker DE, Cochran MD;
XX WPI; 2000-071638/06.
XX N-PSDB; AAX49295.
XX
XX Recombinant fowlpox virus useful as a vaccine for immunizing fowl against
XX Marek's disease, Newcastle disease, Infectious Laryngotracheitis Virus
XX and/or fowlpox.
XX
XX Claim 5; Col 71-74; 56pp; English.
XX
XX The invention relates to a recombinant fowlpox virus (FPV) comprising a
XX foreign DNA inserted into a 4.2 kb EcoRI fragment of the fowlpox virus
XX genome. The foreign DNA is capable of being expressed in a host cell into
XX which the fowlpox virus has been introduced and encodes an antigenic
XX protein. The antigenic protein which may be expressed includes infectious
XX laryngotracheitis virus (ILTV) glycoprotein B (gB) or glycoprotein D (gD),
XX AAY58184, Newcastle disease virus (NDV) haemagglutinin (HN, AAY58182) or
XX fusion (F) protein (AAY58183) and Marek's disease virus gB or gD. The
XX foreign DNA may alternatively encode a cytokine such as chicken
XX myelomonocytic growth factor (CMGF) or chicken interferon (cIFN). The
XX foreign DNA in the recombinant FPV is under the control of one or more
XX synthetic pox promoters, enabling control of strength and timing of
XX heterologous gene expression. The synthetic pox virus promoters that may
XX be used are based on promoters of the vaccinia virus and include early
XX promoter 1 (EPI), late promoter 1 (LPI), EP2 and LP2 (AAZ49291-249294,
XX respectively). The recombinant FPV is generated via homologous
XX recombination between FPV DNA and a homology vector containing the
XX foreign DNA flanked by FPV sequences. The recombinant fowlpox viruses of
XX the invention are used as multivalent live vaccines for immunising fowl
XX against Marek's disease virus, NDV, ILTV and/or fowlpox virus. The
XX present sequence represents NDV fusion (F) protein
XX
XX SQ Sequence 553 AA;
```

Query Match 94.7%; Score 2610; DB 3; Length 553;
Best Local Similarity 93.1%; Pred. No. 6.7e-216;
Matches 515; Conservative 21; Mismatches 17; Indels 0; Gaps 0;

QY 1 MGSRSSTPIPVMLTIVRVALSCVPTSSLDGRPLAAGIVVTCGKAVNIYTSQTGS 60

```
Db 1 MGRSPSTKPPAPMLTIRVALVLSICPANSIDGRPLAAGIIVTGDKAVNIYTSSTGTS 60
Qy 61 IIVKLLPNPKDKEACAKAPLEAYNRTLTLLPLGDSIRRIQESVTTSGGKQGRLLGA 120
Db 61 IIVKLLPNLPKDEACAKAPLDAYNRTLTLLPLGDSIRRIQESVTTSGGKQGRLLGA 120
Qy 121 IIGGAALGVATAAQITTAASALIQANONANILRLKRIIAATNEAVHEVTDGLSOLAVAVG 180
Db 121 IIGVALGVATAAQITTAASALIQANONANILRLKRIIAATNEAVHEVTDGLSOLAVAVG 180
Qy 181 KMQQFVNDQFNKTAQELDCIKITQQVGVNELNLYLTETVFGPQITSPALTIQALYN 240
Db 181 KMQQFVNDQFNKTAQELDCIKITQQVGVNELNLYLTETVFGPQITSPALTIQALYN 240
Qy 241 LAGGNMDDLTKLGVNNQLSSLIIGSLITGNPILYDSQTLIGIQVTLPSVGNLNNMRA 300
Db 241 LAGGNMDDLTKLGVNNQLSSLIIGSLITGNPILYDSQTLIGIQVTLPSVGNLNNMRA 300
Qy 301 TYLETLSVSTTKGFASALVPKVMKGVSVIEELDTSYCIETDLDLYCTRIIVTFPMSPGIY 360
Db 301 TYLETLSVSTTKGFASALVPKVMKGVSVIEELDTSYCIETDLDLYCTRIIVTFPMSPGIY 360
Qy 361 SCLSGNTSACMYSKTEGALTTPYMTLKGSVIANCKMTTCRCADPPGIISQNYGEAVSLID 420
Db 361 SCLSGNTSACMYSKTEGALTTPYMTLKGSVIANCKMTTCRCVNPFGIISQNYGEAVSLID 420
Qy 421 ROSCNVLSIDGITLRLSGEFDATYQKNISIQDSQVITGNLDISTELGNVNNISNALDK 480
Db 421 ROSCNVLSIDGITLRLSGEFDATYQKNISIQDSQVITGNLDISTELGNVNNISNALNK 480
Qy 481 LEESNKLKDVNNKLTSTSTALITYIVLTIVISLVCGLSILVACLYLMYKQAKOQKTLWLG 540
Db 481 LEESNKLKDVNNKLTSTSTALITYIVLTIVISLVCGLSILVACLYLMYKQAKOQKTLWLG 540
Qy 541 NNTLDQMRATTM 553
Db 541 NNTLDQMRATTM 553
```

RESULT 11

AAB36039 standard; protein; 553 AA.

AAB36039;

06-AUG-2003 (revised)

02-MAR-2001 (first entry)

Protein encoded by NDV Sfil fragment.

Fowlpox virus; FPV; antiviral; antibacterial; vaccine;

Newcastle's disease virus; NDV; Marek's disease;

infectious laryngotracheitis.

Newcastle disease virus.

US6136318-A.

24-OCT-2000.

07-JUN-1995; 95US-00486414.

26-FEB-1993; 93US-00024156.

28-FEB-1994; 94WO-US002252.

(JUNK/) JUNKER D E.

(COCH/) COCHRAN M D.

Cochran MD, Junker DE;

WPI: 2000-686071/67.

N-PSDB; AAC67862.

XX New recombinant fowlpox virus useful as vaccines contains foreign DNA
PT inserted into specific non-essential region of the genome.
XX Disclosure; Col 71-74; 56pp; English.
XX The present sequence is provided in a specification relating to a
CC recombinant fowlpox virus (FPV) that comprises a foreign DNA inserted
CC within a 3.5 kb EcoRI fragment of the FPV genomic DNA. The foreign DNA
CC can be expressed in host cells infected with FPV. The recombinant FPV may
CC be used in vaccines to protect animals (especially chickens) against
CC fowlpox and, depending on the source of the foreign DNA, other diseases,
CC particularly Newcastle's disease, Marek's disease or infectious
CC laryngotracheitis. (Updated on 06-AUG-2003 to correct OS field.)
XX Sequence 553 AA;

Query Match 94.7%; Score 2610; DB 3; Length 553;
Best Local Similarity 93.1%; Pred. No. 6.7e-216;
Matches 515; Conservative 21; Mismatches 17; Indels 0; Gaps 0;
Qy 1 MGRSSTRIPVPLMLTIRVALVLSICPANSIDGRPLAAGIIVTGDKAVNIYTSSTGTS 60
Db 1 MGRSSTRIPVPLMLTIRVALVLSICPANSIDGRPLAAGIIVTGDKAVNIYTSSTGTS 60
Qy 61 IIVKLLPNPKDKEACAKAPLEAYNRTLTLLPLGDSIRRIQESVTTSGGKQGRLLGA 120
Db 61 IIVKLLPNLPKDEACAKAPLDAYNRTLTLLPLGDSIRRIQESVTTSGGKQGRLLGA 120
Qy 121 IIGGAALGVATAAQITTAASALIQANONANILRLKRIIAATNEAVHEVTDGLSOLAVAVG 180
Db 121 IIGVALGVATAAQITTAASALIQANONANILRLKRIIAATNEAVHEVTDGLSOLAVAVG 180
Qy 181 KMQQFVNDQFNKTAQELDCIKITQQVGVNELNLYLTETVFGPQITSPALTIQALYN 240
Db 181 KMQQFVNDQFNKTAQELDCIKITQQVGVNELNLYLTETVFGPQITSPALTIQALYN 240
Qy 241 LAGGNMDDLTKLGVNNQLSSLIIGSLITGNPILYDSQTLIGIQVTLPSVGNLNNMRA 300
Db 241 LAGGNMDDLTKLGVNNQLSSLIIGSLITGNPILYDSQTLIGIQVTLPSVGNLNNMRA 300
Qy 301 TYLETLSVSTTKGFASALVPKVMKGVSVIEELDTSYCIETDLDLYCTRIIVTFPMSPGIY 360
Db 301 TYLETLSVSTTKGFASALVPKVMKGVSVIEELDTSYCIETDLDLYCTRIIVTFPMSPGIY 360
Qy 361 SCLSGNTSACMYSKTEGALTTPYMTLKGSVIANCKMTTCRCADPPGIISQNYGEAVSLID 420
Db 361 SCLSGNTSACMYSKTEGALTTPYMTLKGSVIANCKMTTCRCVNPFGIISQNYGEAVSLID 420
Qy 421 ROSCNVLSIDGITLRLSGEFDATYQKNISIQDSQVITGNLDISTELGNVNNISNALDK 480
Db 421 ROSCNVLSIDGITLRLSGEFDATYQKNISIQDSQVITGNLDISTELGNVNNISNALNK 480
Qy 481 LEESNKLKDVNNKLTSTSTALITYIVLTIVISLVCGLSILVACLYLMYKQAKOQKTLWLG 540
Db 481 LEESNKLKDVNNKLTSTSTALITYIVLTIVISLVCGLSILVACLYLMYKQAKOQKTLWLG 540
Qy 541 NNTLDQMRATTM 553
Db 541 NNTLDQMRATTM 553

RESULT 12

AAR14480

ID AAR14480 standard; protein; 553 AA.

AAR14480;

27-AUG-2003 (revised)

25-MAR-2003 (revised)

27-NOV-1991 (first entry)

Newcastle disease virus immunogenic fusion protein.

Db 421 RHSCNVLSLDGITRLSGFDATYQKNISILDSQVITVGNLDSITELGNVNSISNALNK 4

Db

1 MGSRSSTRIPVPLMLIIIRTALTLSLCIRLTSSLDGRPLAAAGIVVTGDKAVNIYTSSQTGS 60

Qy	61	IIVKLLPNMPKDK	EACAPLEAYNRTLT	TLTLP	LGDSIRRIQESV	TTSGGCKOGR	LICA	120
Db	61	IIVKLLPNMPKDK	EACAPLEAYNRTLT	TLTLP	LGDSIRRIQESV	TTSGGCKOGR	LICA	120
Qy	121	IIGGAALGVATAAQ	ITAAASALIOANQNA	ANILRLKERIAA	TNEAVHEVTDGL	SQSLAVAG	180	
Db	121	IIGGAALGVATAAQ	ITAAASALIOANQNA	ANILRLKERIAA	TNEAVHEVTDGL	SQSLAVAG	180	
Qy	181	KMQQPVNDQFNKTA	QOELDCIKITQOQV	VELNLYLT	TVFGPQITSPAL	TOLTITQALYN	240	
Db	181	KMQQPVNDQFNKTA	QOELDCIKITQOQV	VELNLYLT	TVFGPQITSPAL	TOLTITQALYN	240	
Qy	241	LAGNMDDYLLTKL	GVGNQNLSSLIGSL	ITGNPILYDSOT	LLGHTVLP	SGVGNLNNRA	300	
Db	241	LAGNMDDYLLTKL	GVGNQNLSSLIGSL	ITGNPILYDSOT	LLGHTVLP	SGVGNLNNRA	300	
Qy	301	TYLETLSVSTTKGF	ASALVPKVMKGVSI	BELDTSYCIETD	LDLYCYTRIVTFP	MSPGIY	360	
Db	301	TYLETLSVSTTKGF	ASALVPKVMKGVSI	BELDTSYCIETD	LDLYCYTRIVTFP	MSPGIY	360	
Qy	361	SLCSGNTSACMYSK	TEGALTPPYMTL	KGSVIANCQMTTCR	CADPPGIIISQNYGE	AVSLID	420	
Db	361	SLCSGNTSACMYSK	TEGALTPPYMTL	KGSVIANCQMTTCR	CADPPGIIISQNYGE	AVSLID	420	
Qy	421	RQSCNVLSDGITL	RLSGEFATYQKNIS	IODSQVIVTGNL	DISTELGNVANSISNAL	DK	480	
Db	421	RQSCNVLSDGITL	RLSGEFATYQKNIS	IODSQVIVTGNL	DISTELGNVANSISNAL	DK	480	
Qy	481	LEESNKLDKVNVLK	TSTSAITIVLT	VISLVCGILSLV	ACVILMYKQAKOQKTL	WLWG	540	
Db	481	LEESNKLDKVNVLK	TSTSAITIVLT	VISLVCGILSLV	ACVILMYKQAKOQKTL	WLWG	540	
Qy	541	NTLDDQMRATTQM	553					
Db	541	NTLDDQMRATTKI	553					

RESULT 14

AAAP70176	AAAP70176 standard; protein; 553 AA.
ID	AAAP70176 standard; protein; 553 AA.
XX	AC
XX	AAAP70176;
XX	AC
XX	27-AUG-2003 (revised)
DT	25-MAR-2003 (revised)
DT	03-APR-1991 (first entry)
DT	DT
XX	Sequence of Newcastle Disease Virus (NDV) F polypeptide.
DE	XX
XX	XX
XX	Epitope; probe; diagnosis.
KW	XX
XX	XX
OS	Newcastle disease virus.
XX	XX
XX	EP227414-A.
PN	XX
PD	01-JUL-1987.
PD	XX
XX	XX
PF	16-DEC-1986; 86EP-00309804.
XX	XX
XX	18-DEC-1985; 85GB-00031147.
PR	14-APR-1986; 86GB-00009037.
PR	15-JUL-1986; 86US-00885765.
PR	XX
PA	(NATR) NAT RES DEV CORP.
PA	XX
PI	Bingham RW, Chambers P, Emmerson PT, Millar NG;
PI	XX
XX	WPI; 1987-179630/26.
DR	N-PSDB; AAAN70261.
DR	XX
XX	Newcastle disease virus gene clones - comprise polynucleotide (s) encoding the HN and/or F protein of Newcastle disease virus RNA.
XX	XX
PT	XX
PT	XX

XX PS Example; Page 11-16; 22pp; English.

XX CC An artificial polynucleotide encoding an HN and/or F polypeptide of

XX CC Newcastle Disease Virus (NDV) DNA, a bioprecursor of the polypeptide, or

XX CC an epitopic portion of the polypeptide or an artificial nucleotide

XX CC complementary to the polynucleotide are claimed. The polynucleotides are

XX CC useful for preparing a probe for extracting similar genes from a gene

XX CC library or for identifying the presence of NDV virions in a sample obtd.

XX CC from poultry. (Updated on 25-MAR-2003 to correct PA field.) (Updated on

XX CC 27-AUG-2003 to correct OS field.)

XX SQ Sequence 553 AA;

Query Match 94.4%; Score 2603; DB 1; Length 553;

Best Local Similarity 93.5%; Pred. No. 2.7e-215;

Matches 517; Conservative 19; Mismatches 17; Indels 0; Gaps 0;

QY 1 MGRSSSTRIPEVPLMLTVRVALALSCVPTSSLDGRPLAAGIVVTGDKAVNIYTSSTGS 60

DB 1 MGRPSTKNPVPMMLTVRVALVLSVICPANSIDGRPLAAGIVVTGDKAVNIYTSSTGS 60

QY 61 IIVKLLPNMKDKEACAKAPLEAYNRTLTLLTPLGDSIRRIQESVTTSGGKQRLGA 120

DB 61 IIVKLLPNLKDEACAKAPLDAYNRTLTLLTPLGDSIRRIQESVTTSGRQKRFGA 120

QY 121 IIGGALGVATRAQITHAASALIQANQAAAILRLKERIAATNBAVHEVTDGLSQLAVAG 180

DB 121 IIGGALGVATRAQITAAALIOAKQNAANILRLKESIAATNBAVHEVTDGLSQLAVAG 180

QY 181 KMQQFVNDQFNKTAQELDCIKITCOQGVNELNLVLTTLTTFVFGPQITSPALTIQALYN 240

DB 181 KMQQFVNDQFNKTAQELGCIIRIAQQGVNELNLVLTTLTTFVFGPQITSPALNKTIQALYN 240

QY 241 LAGNNMDYLLTKLGVGNQNLSSLIGSLGITGNPILYDSQTLGLGIQVTLPSVGNLNNMRA 300

DB 241 LAGNNMDYLLTKLGVGNQNLSSLIGSLGITGNPILYDSQTLGLGIQVTLPSVGNLNNMRA 300

QY 301 TYLETLSVSTTKGFASALVPKVMKVGSVIEELDTSYCIETDLDLYCTRIVTTPMSPGIY 360

DB 301 TYLETLSVSTRGFASALVPKVVTQVGSVIEELDTSYCIETDLDLYCTRIVTTPMSPGIY 360

QY 361 SCLSGNTSACMYSKTEGALTTPWMTLKGSVIANCKMTTCRCADPGIISONTGEAVSLID 420

DB 361 SCLSGNTSACMYSKTEGALTTPWMTLKGSVIANCKMTTCRCVNPPIIISONTGEAVSLID 420

QY 421 QSCNVLSLDGILRLSGBEDATYQKNISIQDSQVITVGNLIDISTELGNVNNISINALDK 480

DB 421 QSCNVLSLDGILRLSGBEDATYQKNISIQDSQVITVGNLIDISTELGNVNNISINALNK 480

QY 481 LEESSNKLKDVNKLTTSTSALITYVLTVISLVCGTSLVLAACLYMKQAKQKTLILWLG 540

DB 481 LEESSNKLKDVNKLTTSTSALITYVLTVISLVCGTSLVLAACLYMKQAKQKTLILWLG 540

QY 541 NNTLDQMRATTKM 553

DB 541 NNTLDQMRATTKM 553

RESULT 15

ABG31709

ID ABG31709 standard; protein; 564 AA.

XX AC

XX ABG31709;

XX AC

15-NOV-2002 (first entry)

XX DE Newcastle disease virus (NDV) fusion protein.

XX DE

XX Newcastle disease virus; NDV; novel recombinant avian herpesvirus; NAHV;

XX KW herpes virus of turkeys; HVT; Marek's disease; Newcastle disease;

XX KW infectious laryngotracheitis; virucide; immunostimulant; vaccine.

XX XX

	OS	Newcastle disease virus.			
XX	Key	Location/Qualifiers			
FH	Misc-difference	54			
FT	/label=	unknown			
FT	/note=	"Encoded by CTN"			
XX	US2002081316-A1.				
PX					
PD	27-JUN-2002.				
XX					
PF	14-JUN-2001; 2001US-00881457.				
XX					
PR	12-JUN-1992; 92US-00898087.				
PR	26-FEB-1993; 93US-00023610.				
PR	14-JUN-1993; 93WO-US0005681.				
PR	09-AUG-1994; 94US-00288065.				
PR	09-AUG-1995; 95WO-US010245.				
PR	13-JUN-1996; 96US-00663566.				
PR	21-FEB-1997; 97US-00804372.				

Search completed: April 18, 2004, 01:23:38
Job time : 103 secs

XX Cochran MD, Cook SM, Wild MA;
PI
XX
XX WPI; 2002-635456/68.
DR N-PSDB; ABK90556.
XX
XX
XX Novel recombinant avian herpesvirus comprising unique long and repeat
PT viral genome regions of herpes virus of turkeys, unique short viral
PT genome region of Marek's disease virus, and optional foreign DNA
PT sequence.
XX
XX Disclosure; Page 14-16; 26pp; English.
PS
XX
XX The invention relates to a novel recombinant avian herpesvirus (NAHV)
CC comprising a herpes virus of turkeys (HVT) unique long (UL) and repeat
CC viral genome region and a Marek's disease virus unique short (US) viral
CC genome region where at least one foreign DNA sequence is inserted within
CC a US2 gene of the US region of the NAHV, and is capable of being
CC expressed in a host cell. NAHV is useful for producing vaccines used for
CC immunising an avian species against Newcastle disease, infectious
CC laryngotracheitis and Marek's disease. This sequence represents a
CC Newcastle disease virus (NDV) fusion protein
XX
XX Sequence 564 AA;
SQ

Query Match	90.4%;	Score	2493.5;	DB 5;	Length	564;		
Best Local Similarity	89.7%;	Pred.	No. 7.8e-206;					
Matches	496;	Conservative	24;	Mismatches	32;	Indels	1; Gaps	1;

Qy	1	MGSSSTPIPVPLMLTVRVALALSCVPTSSIDGRPLAAGIVTGDKAVNIYTSQTGS	60
Dd	13	MGSRPSTKNPAPMMLTRVALVLSCICPANSIDGRPLAAAGXWLQETQ-K-STYTFHPQV	71
		: : : :	
Qy	61	IIVKLLPNMPDKKACAKAPLEAYNRITLTTLTPLGDSIRRIQRSVTSSGGKGQRLLGA	120
Dd	72	NHIIKLPLNPKDKEACAKAPLDAYNRITLTTLTPLGDSIRRIQRSVTSSGGGROQRLLGA	131
		: : : :	
Qy	121	IIGGAALGVATAAQITTAASALTQAQNAAANILRLKERIAATNEAVEHTDGLSOLAVVG	180
Dd	132	IIGGVALGVATAAQITAAAALIQAQNAAANILRLKESIAATNEAVEHTDGLSOLAVVG	191
		: : : :	
Qy	181	KMQQFVNDFNKTAQLDCIKITQQGVVELNLXLTELTTVFQPQITSPALTLQIALYN	240
Dd	192	KMQQFVNDFNKTAQLDCIKIAQQGVVELNLXLTESTTTVFQPQITSPALNKLIQIALYN	251
		: : : :	
Qy	241	LAGGNMDYLLTKLGVGNNSLSLIGSLGITNPILYDSCTOLLGIQVTLPSVGMNNMRA	300
Dd	252	LAGGNMDYLLTKLGTGNNSLSLIGSLGITNPILYDSCTOLLGIQVTLPSVGMNNMRA	311
		: : : :	

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